

Table 1

## Phages against human and animal pathogenic bacteria

5

Pathogen name	Phage name	Catalog#	Origin/reference
<i>Acinetobacter calcoaceticus</i>	A3/2 A10/45 A36 B9GP B <sub>9</sub> PP BS46 E13 E14 531		Felix d'Herelle Reference Centre, Quebec, Quebec
	Ap3 P78		J. Bacteriol 1984. 157: 179-183 J. Gen. Microbiol 1986.132: 2633-2636
<i>Acinetobacter haemolyticus</i>	2213/73		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Acinetobacter johnsonii</i>	133		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Acinetobacter sp.</i>	BP1		J. Virol. 1968.2:716-722
	G4, HP2, HP3 & HP4		Can. J. Microbiol. 1966.12:1023-1030 & J. Virol. 1974.13:46-52 & Arch. Virol. 1994.135:345-354
	A1, A4, A9 & 196		Arch. Virol. 1994.135:345-354
	HP1		Can. J. Microbiol. 1966.12:1023-1030
	A19, A23, A29, A31, A33, A34, A3759 & 2845		J. Microsc (Paris) 1973.16:215-224 & CR. Hebdo Seances Acad. Sci. Ser D. Sci Natur (Paris) 278:1907-1909 & Arch. Virol. 1994.135:345-354 & Rev. Can. Biol. 1970.29:317-320
<i>Actinobacillus actinomycetecomitans</i>	φAa		FEMS Microbiol Lett 1994. 119:329-337
	φAa17		Infect. Immun. 1982. 35: 343-349
	Aaφ23		Mol. Gen. Genet 1998.258: 323-325
	Aaφ247		Oral Microbiol. Immunol 1997.12: 40-46
<i>Actinomyces viscosus</i>	Av-1	43146-B1	The American Type Culture Collection
	AV-2, AV-3 & 1281		Infect. Immun. 1985.48:228-233
	BF307 & CT7		Infect. Immun. 1988.56:54-59
	phi225		Plasmid 1997.37:141-153
<i>Aeromonas hydrophila</i>	PM2** & PM3		FEMS Microbiol. Lett. 1990.57:277-282
SD-63311.4			

	Aeh1 Aeh2 PM4 PM5 PM6 T7-ah		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Aeromonas salmonicida</i>	3 25 29 31 32 40RR <sub>2,8</sub> <sup>t</sup> 43 51 56 59.1 65 Asp37 55R.1		Felix d'Herelle Reference Centre, Quebec, Quebec  Can. J. Microbiol. 1983. 29: 1458-1461
<i>Alteromonas espejiana</i>	PM2**	27025-B1	The American Type Culture Collection
<i>Asticcacaulis biprosthecum</i>	B1a		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Asticcacaulis excentricus</i>	φAc20 φAc21 φAc24	15261-B1 15261-B2 15261-B3	The American Type Culture Collection
<i>Azotobacter vinelandii</i>	A12 A14 A21 A31 A41 PAV1	12518-B1 12518-B4 12518-B5 12518-B9 12518-B10 13705-B1	The American Type Culture Collection
<i>Azotobacter sp.</i>	A12		Virology 1972.49:439-452
<i>Bacteroides fragilis</i>	Bf-1		Rev. Infect. Dis. 1979. 1: 325-336
	B40-8		FEMS Microbiol. Lett. 1991. 66: 61-67
	HSP40		Appl. Environ. Microbiol. 1989. 55: 2696-2701
	phiA1		Zentralbl.bakteriol.1972.222:57-63
<i>Bdellovibrio bacteriovorus</i>	MAC-1		J. Gen. Microbiol. 1987. 133: 3065-3070
<i>Bdellovibrio sp.</i>	VL-1		J.Virol.1973.12:1522-1533
<i>Bordetella brochiseptica</i>	214		Zh.Mikrobiol.Epidemiol.Immuno. 1987.5:9-13
<i>Bordetella parapertussis</i>	L-1 Tohama		Felix d'Herelle Reference Centre, Quebec, Quebec
	phiT		Mol. Gen. Mikrobiol. Virusol. 1988.4: 22-25
	134		Zh.Mikrobiol.Epidemiol.Immuno. 1987.5:9-13
	41405		Zh.Mikrobiol.Epidemiol.Immuno. 1987.5:9-13

<i>Brucella abortus</i>	S708 Fi75/13		Felix d'Herelle Reference Centre, Quebec, Quebec
	Tbilisi 10/I 24/II 212/XV 371/XXIX	23448-B1 23448-B2 23448-B3 17385-B1 17385-B2	The American Type Culture Collection
	BK-2, TB & Fi**		Zh.Mikrobiol.Epidemiol.Immunobiol.1983.2: 48-52
	R/c & R/O		Dev. Biol. Stand. 1984.56: 55-62
	R/c		Dev. Biol. Stand. 1984.56: 55-62
<i>Brucella canis</i>	R/c		Dev. Biol. Stand. 1984.56: 55-62
<i>Brucella melitensis</i>	BK-2	23456-B1	The American Type Culture Collection
<i>Brucella suis</i>	Wb		Zentralbl.Veterinarmed.1975.22:866-867
	Fi** & TB		Zh.Mikrobiol.Epidemiol.Immunobiol.1983.2: 48-52
<i>Brucella sp.</i>	Np (Nepean) & Iz		Can. J. Vet. Res. 1989.53: 319-325
	Iz-1		Res. Vet. Sci. 1988. 44: 45-49
	R		Zh.Mikrtobiol.Epidemiol.Immunobiol.1983.2: 48
<i>Campylobacter coli</i>	17	43133-B1	The American Type Culture Collection
	18	43134-B1	
<i>Campylobacter coli</i> (Cont'd)	19	43135-B1	The American Type Culture Collection
	20	43136-B1	
<i>Campylobacter jejuni</i>	1	35918-B1	The American Type Culture Collection
	2	35919-B1	
	3	35920-B1	
	4	35921-B1	
	5	35918-B2	
	6	35920-B2	
	7	35922-B2	
	8	35923-B1	
	9	35924-B1	
	10	35925-B1	
	11	35925-B2	
	12	35922-B2	
	13	35924-B2	
	14	35922-B3	
	17	43133-B1	
	18	43134-B1	
	19	43135-B1	
	20	43136-B1	
<i>Campylobacter</i> ( <i>Helicobacter</i> ) <i>pylori</i>	HP1		J. Med. Microbiol.1993. 38: 245-249
<i>Chlamydia psittaci</i>	Chp1**		J. Gen. Virol. 1989. 70: 3381-3390
<i>Clostridium</i> <i>acetobutylicum</i>	CAK-1		J.Bacteriol.1993.175:3838-3843
<i>Clostridium botulinum</i>	C** & D**		Nucleic Acids Res.1990.18:1291
	C-ST**		Bioch.Biophys.res.Communi.1990.171.1304- 1311
	$\alpha 1$ & $\alpha 2$		Microbiol.immunol.1981.25:915-927
SD-63311.4			

	d-16 phi**, d-1', CE $\beta$ & CE $\gamma$		J.Vet.Med.Sci.1992.54:675-684
<i>Clostridium difficile</i>	41 & 56		J. Clini.Microbiol. 1985.21:251-254
<i>Clostridium perfringens</i>	PF1, PF2, PF3 & PF4		Rev.Can.Biol.1977.36:205-215
	$\phi$ 29** & $\phi$ 59		FEMS Microbiol.Lett. 1990.54:323-326
<i>Clostridium sporogenes</i>	J 59 70 71 72S 72L	8074-B1 17886-B1 17886-B3 17886-B4 17886-B5 17886-B6	The American Type Culture Collection
<i>Clostridium tetani</i>	A & B		Rev.Can.Biol.1978.37:43-46
<i>Corynebacterium diphtheriae</i>	BF, $\phi$ 9 & $\phi$ 984		Vopr.Virusol.1986.31:577-584
<i>Corynebacterium pseudotuberculosis</i>	NN	12319-B1	The American Type Culture Collection
<i>Corynebacterium sp</i>	DLC 2921/49	12052-B1	The American Type Culture Collection
<i>Enterococcus faecalis</i>	42	19948-B1	The American Type Culture Collection
<i>Enterococcus faecium</i>	113	19950-B1	The American Type Culture Collection
	124	19953-b2	
	133	19953-B1	

<i>Escherichia coli</i>	AP211	11303-B14	The American Type Culture Collection
	BG3	11303-B10	
	C33	11303-B21	
	C36	8677-B1	
	C204	11303-B13	
	E1	13706-B4	
<i>Escherichia coli</i> (Cont'd)	f1**	15766-B1	The American Type Culture Collection
	f2**	15766-B1	
	FCZ	1242-B5	
	fd**	15669-B2	
	fr**	15767-B1	
	G178	11303-B16	
	If1**	27-65-B1	
	If2	25065-B2	
	M13**	15669-B1	
	MS2**	15597-B1	
	MU9	21816-B1	
	Mu-1	23724-B9	
	Ox6	15593-B1	
	P1**	25404-B1	
	P4 sid <sub>1</sub> **	29746-B1	
	Q-β**	23631-B1	
	R17**	25868-B1	
	Z1K/1	25298-B1	
	ZJ/2	25298-B2	
	rA105	11303-B37	
	rEDa41	11303-B24	
	rED220	11303-B26	
	rEDb44	11303-B27	
	rEDb45	11303-B28	
	rEDb50	11303-B29	
	rH23	11303-B30	
	rH88	11303-B33	
	rJ3	11303-B31	
	r71	11303-B25	
	r187	11303-B35	
	r196	11303-B34	
	r638	11303-B36	
	r1589	11303-B32	
	S13**	13706-B5	
	T <sub>1</sub> **	11303-B1	
	T <sub>2</sub> **	11303-B2	
	T <sub>3</sub> **	11303-B3	
	T <sub>4</sub> **	11303-B4	
	T <sub>4</sub> amA453	35060-B1	
	T <sub>4</sub> amB17	35060-B2	
	T <sub>4</sub> amN120	35060-B3	
	T5**	11303-B5	
	T6**	11303-B6	
	T7**	11303-B7	
	T <sub>7</sub> M	11303-B38	
SD-63311.4	5	12141-B1	
	6A	12144-B3	

<i>Escherichia coli</i> (Cont'd)	250	11303-B20	The American Type Culture Collection
	547	11303-B17	
	UV1	11303-B15	
	UV47	11303-B11	
	UV375	11303-B18	
	$\alpha 3^{**}$	13706-B2	
	$\lambda^{**}$	23724-B2	
	$\lambda$ C-17	23724-B1	
	$\lambda$ sus P-3	23724-B3	
	$\lambda$ sus R-5	23724-B4	
	$\lambda$ sus J-6	23724-B5	
	$\lambda$ sus O-8	23724-B6	
	$\lambda$ sus A-11	23724-B7	
	$\lambda$ ind <sup>-</sup>	23724-B8	
	$\phi 92$	35860-B1	
	$\phi R$	13706-B3	
	$\phi V-1$	15597-B2	
	$\phi X174^{**}$	13706-B1	
	$\phi Xcs70am-3$	49696-B1	
	G4 <sup>**</sup> & $\phi K^{**}$		Biochim.Biophysica Acta.1992.1130:277-288
	BF23 <sup>**</sup>		J.Bacteriol.1977.129:265-275
	Mu1		J.Ultrastruct.Res.1966.14:441-448
	Hp17		J.Mol.Biol.1991.218:705-721
	K3 <sup>**</sup> & Ox2 <sup>**</sup>		FEBS Lett.1987.215:145-150
	Rb18 <sup>**</sup> , Rb51 & Rb69 <sup>**</sup>		J.Bacteriol.1990.172:180-186
	H1 <sup>**</sup> , H3, H8, K9, K18 & Ox1		Mol.Gen.Genet.1990.221:491-494
	M1 <sup>**</sup> , Tu1a <sup>**</sup> & Tu1b <sup>**</sup>		J.Mol.Biol.1987.196:165-174
	K10		J.Bacteriol.1979.140:680-686
	Qsr'		J.Bacteriol.1985.162:256-262
	B278		J.Gen.Microbiol.1988.134:1333-1338
	phi 80 <sup>**</sup>		FEMS Microbiol.Lett.1994.119:71-76
	phi m173		Genetika 1985.21:673-675
	tf-1		J.Gen.Microbiol.1987.133:953-960
	P4 & phiR73		Mol.Microbiol.1995.18:201-208
	I <sub>2</sub> -2		J.Gen.Microbiol.1982.128:2797-2804
	PRD1		Virology 1990.177:445-451
	K3hx		Mol.Gen.Genet.1987.206:110-115
	933J <sup>**</sup> & 933W <sup>**</sup>		Infect.Immunity.1986.53:135-140
	H19-B <sup>**</sup>		J.Bacteriol.1987.169:4308-4312
	Tcp-111		Zentralbnl.Bakteriol.Mikrobiol.Hyg.1988.270:41-51
	N4 <sup>**</sup>		Vet.Microbiol.1992.30:203-212
	Phi 80 trp		Ann.Inst.Pasteur.1971.120:121-125
	Obeta 1		J.Bacteriol.1978.133:172-177

<i>Escherichia coli</i> (Cont'd)	P1CM	J.Gen.Microbiol.1978.107:73-83
	PA-2**	J.Bacteriol.1990.172:1660-1662
	186**	Mol.Gen.Genet.1982.187:87-95
	186.IX.B	Mol.Microbiol.1992.6:2629-2642
	21**	Virology 1983.129:484-489
	P4**	MicrobiolRev.1993.57:683-702
	82**	J.Biol.Chem.1987.262:11721-11725
	PSP3	J.Bacteriol.1996.178:5668-5675
	HK022**	Nucleic Acids Res.1994.22:354-356
	D108**	Nucleic Acids Res.1986.14:3813-3825
	Rb49	J.Mol.Biol.1997.267:237-249
	Ike**	J.Mol.Biol.1985.181:27-39
	P22dis	Mol.Gen.Genet.1978.166:233-243
	N15**	J.Bacteriol.1996.178:1484-1486
	If1**	Proc.R.Soc.Lond.B.Biol.Sci.1991.245:23-30
	Stx2Phi-I & Stx2Phi-II	Infect.Immun.1998.66:4100-4107
	18	Virology 1987.156:122-126
	X	J.Gen.Microbiol.1981.126:389-396
	AC3	Mol.Microbiol.1991.5:715-725
	BW-1 C-1 E920g Esc-7-11 H19J Haiti HK243 Iα K20 K30 KL <sub>3</sub> M Mu** O103 O157:H7 P1D pt1 PilHα PR64FS PR772 SS4 β4Q λvir** Ω8 09-1 92	Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Haemophilus influenzae</i>	HP1**	Nucleic Acids Res. 1996.24:2360-2368
	S2**	Gene 1997. 196: 139-144

<i>Halobacterium cutirubrum</i>	S45		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Halobacterium halobium</i>	φH & φN		Felix d'Herelle Reference Centre, Quebec, Quebec
	Hh1 & Hh3		Can.J.Microbiol.1982.28:916-921
<i>Halobacterium salinarium</i>	Phi H		Biol.Chem.Hoppe Seyler 1994.375:747-757
<i>Klebsiella oxytoca</i>	tf-1		J.Gen.Microbiol.1987.133:953-960
<i>Klebsiella pneumoniae</i>	60 92	23356-B1 23357-B1	The American Type Culture Collection
	K19Q		Felix d'Herelle Reference Centre, Quebec, Quebec
	FC3-1 & FC3-9		Can.J.Microbiol.1991.37:270-275
	FC3-10		FEMS Microbiol.Lett.1991.67:291-297
<i>Klebsiella sp.</i>	K11**		Mol.Gen.Genet. 1990.221:283-286
<i>Leptospira sp.</i>	LE1, LE3 & LE4		Res.Microbiol.1990.141:1131-1138
<i>Listeria monocytogenes</i>	243	23074-B1	The American Type Culture Collection
	197,1313 & 9425		Appl.Environ.Microbiol.1997.63:3374-3377
	H387 & H387-A		Appl.Environ.Microbiol.1993.59:2914-2917
	5775,6223 & 12682		APMIS.1993.101:160-167
	2389, 2671, 4211 & 2685		Intervirology 1994.37:31-35 & Zentralbl.Bakteriol.Mikrobiol.Hyg.1986.261:12-28
	4b, 4ab, 4g & 3c		Ann.Microbiol (Paris) 1977.128:185-198
	A118, A500 & A511**		Mol.Microbiol. 1995.16:1231-1241-992
	1, 3, 4, 5, 6, 7, 8, 9, 10, 11, 14, 15, 16, 17, 19 & 20		Ann.Microbiol. (Paris) 1979.130B:179-189
	1/2a, 1/2b, 3c, 4ab, 6a & 6b		Clin.Invest.Med.1984.7:229-232
	φLMUP35 2685		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Listeria innocua</i>	4211		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Micrococcus luteus</i>	N1 N3 N4 N8	4698-B1 4698-B4 4698-2 4698-B3	The American Type Culture Collection
	N17		Can.J.Microbiol. 1979.25:1027-1035



<i>Mycobacterium smegmatis</i>	BK-3	27203-B1	The American Type Culture Collection
	Bo1**	27204-B1	
	Bo 6	27205-B1	
	Bo 6II	27205-B2	
	Bo 6III	27205-B3	
	Mc-2	607-B6	
	Mc-4	607-B7	
	NN	11727-B1	
	Phagus laticola	11759-B1	
	R1	607-B1	
	33D	HER 317	Felix d'Herelle Refrence
	BK1	HER 330	Centre, Quebec, Quebec
	Clark	HER 333	
	DNA III	HER 335	
	Legendre	HER 334	
	Leo	HER 331	
	Roy	HER 316	
	Sedge	HER 332	
	L5**		Mol.Microbiol.1993.7:395-405
	D29		J.Mol.Biol.1998.279:143-164
	L1		Proc.Natl.Acad.Sci USA.1988.84:2833-2837
	I3		Mol.Biol.Rep. 1981.30:11-15
	TM4		Proc.Natl.Acad.Sci.USA 1997.94:10961-10966
	29M, 31M, 122, 154, 37, 29D, 46, 139, 110, 141, 74D, AG1 & DS6A		Arch.Virol.1993.133:39-49 & Am.Rev.Respir.Dis.1975.112:17-22
<i>Mycobacterium fortuitum</i>	NN	23052-B1	The American Type Culture Collection
	Bo 4	27207-B1	
	Bo 7	27207-B2	
<i>Mycobacterium leprae</i>	BK1, Clark, Sedge, Baits, Watson & D29		Ann.Microbiol. (Paris) 1982.133:93-97
<i>Mycobacterium tuberculosis</i>	LG	25618-B1	The American Type Culture Collection
	DS6A	25618-B2	
	D-34	4243-B1	
	110, 139 & 33D		Arch.Virol.1993.133:39-49
	AG1, GS4E, BG1, PH & BK1		The Biology of Mycobacteria. Academic Press, Toronto 1982 (Ratledge & Stanford) 1982.309-351
<i>Mycobacterium sp</i>	Phagus pellegrini	11760-B1	The American Type Collection Culture
	NN	11761-B1	
	B1	23239-B1	
	TM4, ph60, ph72, PhAE39, phAE40 & Bxb1		Microbiology 1995.141:1173-1181
	C2		Experientia 1969.25:1112-1113

	18 & I15		J.Gen.Virol.1987.68:949-956
	63		Gruzlica 1968.36:617-622
	phlei & butyricum		J.Gen.Virol.1975.29:235-238
	MyF3P-59a		Z.Allg.Mikrobiol.1968.8:29-37
	Bo2a		J.Gen.Virol.1973.20:75-87
	D4,D28 & D32		J.Exptl.Med.1966.123:327-340
	HC		J.Bacteriol.1963.86:608-609
<i>Mycobacterium vaccae</i>	B5	15483-B1	The American Type Culture Collection
<i>Mycobacterium phlei</i>	NN NN Bo 2 Bo 2h Bo 3	11728-B1 11758-B1 27086-B2 27086-B1 27206 B1	The American Type Culture Collection
<i>Mycoplasma arthritidis</i>	MAV1**		Infect.Immunity.1995.63:4016-4023
<i>Mycoplasma hyorhinis</i>	Hr-1		Arch.Virol.1983.77:81-85
<i>Mycoplasma pneumoniae</i>	Br-1		Arch.Virol.1983.75:1-15
<i>Mycoplasma pulmonis</i>	P1		Plasmid 1995. 33: 41-49
<i>Mycoplasma sp.</i>	MV-01		J.Gen.Microbiol.1985:131:3117-3126
	L1		J. Virol.1986.59:584-590
	L2**		Gene 1994. 141: 1-8
	L3 (MV-L3)		Microbios 1990. 64: 111-125
	MAV-1		Infection& Immunity 1995. 63: 4016-4023
	20-P		Med.Biol.1982.60:116-120
	MV-L2 & MV-Ig-pS2-L172		Arch.Virol.1979.61:289-296
	MV-Ig-L 172		Acta.Virol.1978.22:443-450
	BN1		J.Gen.Virol.1979.42:315-322
	MVL51		Virology 1973.55:118-126
	MVL1, MVL52 & MVL51		Science 1971.173:725-727
<i>Neisseria perflava</i>	NP-1		J.Clin.Microbiol.1976. 4:87-91
<i>Nocardia erythropolis</i>	φC		J.Gen.Virol.1974.23:247-254
	φEC		J.Bacteriol.1976.126:1104-1107
<i>Pasteurella multocida</i>	B225		Arch.Exp.Veterinarmed.1981.35:433-436
	B939a		Am.J.Vet.Res.1978.39:1565-1566
	Nos.115, 32, 967 & 1075		Vet.Med.Nauki. 1977.14:33-36
<i>Propionibacterium acnes</i>	NN	29399-B1	The American Type Collection Culture

<i>Pseudomonas aeruginosa</i>	1	12175-B1	The American Type Culture Collection
	2	12175-B2	
	2A	12175-B3	
	2B	12175-B4	
	11	14205-B1	
	16	14206-B1	
	24	14207-B1	
	27	14208-B1	
	44	14209-B1	
	73	14210-B1	
	95	14211-B1	
	109	14212-B1	
	113	14213-B1	
	249	14214-B1	
	B3	15692-B1	
	Hoff 2	14203-B1	
	Hoff 3	14204-B1	
	Pa	12055-B1	
	Pb	12055-B2	
	PB-1	15692-B3	
	Pc	12055-B3	
	Pf	25102-B1	
	PP7**	15692-B2	
	SD1-M, $\phi$ w14, 7 & 31		Felix d'Herelle Reference Centre, Quebec, Quebec
	Pf3**		J.Virol.1983.47:221-223
	$\phi$ -MC		Can.J.Microbiol.1969.15:1179-1186
	Pf1**		J.Mol.Biol.1991.218:349-364
	PR4**		J.Gen.Virol.1979.43:583-592
	A7		J.Bacteriol.1992.174:2407-2411
	KF1		J.Biochem.1983.93:61-71
	$\phi$ CTX**		Mol.Microbiol.1993.4:1703-1709
	f2**		J.Virol.1977.24:135-141

	<p>φKZ, 21, φNZ, PMN17, PTB80, 68, PB-1, E79, 16, 109, 352, 1214, F8, 71, 337, M4, φC17, SL2, B17, Li-24, φmnP78, PS17**, φ1, 73, M6, Li-2, 7, φmnF82, PTB2, PTB20, PTB42, φKF77, 31, PTB21, 119x, φPLS27, B3, 258, Hw12, PM57, PM62, PM105, 148, PM681, 198, 218, 222, 242, 246, PC131, φC11, SL5, D3112**, Jb19, F7, PM69, PM13, PM61, PM113, φ240, 249 &amp; 269</p>		Arch.Virol.1993.131:141-151
<i>Pseudomonas aeruginosa</i> (Cont'd)	<p>297, 309, 318, 11, PH51, 342, 351, PH93, 357-1, 13, 14, PC11-1, 267, D 3**, PC351, KF, PM63, PH132, , I°, φX, 400-1, 45, SM, SL3, SL1, φ11, F10, φC15, 160, 20, 336, 350, φC5, φC11-1, φC13, 295, , SL4, G101, F116, B26, φBS, 53, 145, 284 &amp; 308</p>		Arch.Virol.1993.131:141-151
<i>Pseudomonas cepacia</i>	42 & 83-24		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Pseudomonas fragi</i>	ps1 wy	27362-B1 27363 B1	The American Type Culture Collection
<i>Pseudomonas phaseolicola</i>	φ6		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Pseudomonas putida</i>	gh-1	12633-B1	The American Type Culture Collection

<i>Pseudomonas syringae</i>	NN φ6	40492-B1 21781-B1	The American Type Culture Collection
<i>Pseudomonas sp.</i>	PPs-G3	49780-B1	The American Type Culture Collection
<i>Salmonella bareilly</i>	Sab 2		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Salmonella enteritidis</i>	1, 2, 3 & 6		Epidemiol. Infect. 1995.114:227-236
	2a, 3a, 4a, 5a, 6a, 7a, 8a, 9a, 15, 19, 20 & 21**		Vet. Med. Nauki. 1975.12:55-60
<i>Salmonella newington</i>	Epsilon 34		J. Struct. Biol. 1995.115:283-289
<i>Salmonella newport</i>	7-11	27869-B1	The American Type Culture Collection
	16-19	27869-B2	
	2.5a		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Salmonella paratyphi</i>	31	19940-B1	The American Type Culture Collection
	Paratyphoid A	12176-B1	
	Jersey		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Salmonella senftenberg</i>	SasL1, SaL2, Sal 3, SaL4, SaL5 & SasL6		Indian J. Med. Res. 1997.105:47-52
<i>Salmonella typhimurium</i>	P22**	19585-B1	The American Type Culture Collection
	SL-1	40282	
	MB78**		J. Virol. 1982.41: 1038-1043
	SE1		J. Gen. Microbiol. 1986.132:1035-1041
	LT2		Virology 1971.45:835-636
	ES18**		Virology 1970.42:621-632
	L**		J. Virol. 1985.56:1034-1036
	P1CM clr-100		Mol. Gen. Genet. 1975.138:113-126
	F22		Genet. Res. 1986.48:139-143
	Fels 1		J. Gen. Virol. 1978.38:263-272
	Fels 2		Genet. Res. 1986.48:139-143
	Px		Mol. Gen. Genet. 1970.108:184-202
	P1kc		Virology 1974.60:503-514
	A3 & A4		J. Bacteriol. 1987.169:1003-1009
	HT		Genet. Res. 1976.27:315-322
<i>Salmonella typhimurium</i> (Cont'd)	IRA		J. Basic Microbiol. 1990.30:707-716
	Mud1		Mol. Gen. Genet. 1986.202:327-330
	P22 (cir4-1, cir5- 1 & cir6-1)		Mol. Gen. Genet. 1984.198:105-109
	BF23**		Mol. Gen. Genet. 1976.147:195-202
	Kb1		J. Bacteriol. 1974.117:907-908
	P221dis		J. Gen. Virol. 1978.41:367-376
	PRD1**		Virology 1990.177:445-451
	L <sub>2</sub> -2**		J. Gen. Microbiol. 1982.128:2797-2804
	tf-1		J. Gen. Microbiol. 1987.133:953-960
	X**		J. Gen. Microbiol. 1981.126:389-396

<i>Salmonella typhosa/typhi</i>	8	19937-B1	The American Type Culture Collection
	23	19938-B1	
	25	19939-B1	
	46	19942-B1	
	53	19943-B1	
	163	19946-B1	
	175	19947-B1	
	ViI	27870-B1	
	ViVI	27870-B2	
	O1		Felix d'Herelle Refrence Centre, Quebec, Quebec
	ViII		Chung Hua Liu Hsing Ping H.T.C.1992.13:288
	j2		J.Gen.Microbiol.1983.129:3395-33400
<i>Salmonella sp.</i>	P3	25957-B1	The American Type Culture Collection
	P4**	25957-B2	
	P9a	25957-B3	
	P9c	25957-B4	
	P10	25957-B5	
	102	19945-B1	
	Chi (χ)	9842-B1	
	R34	97541	
	MG40		Virology 1968.34:521-530
	P14		Microb.Pathog.1990.8:393-402
	PSP3		Virology 1992.188:414
	Ike**		Zentralbl.Bakteriol.1976.234:294-304
	P27 & 9NA		J.Virol.1986.12:921-931
<i>Sphaerotilus natans</i>	SN1		Appl.Environ.Microbiol.1979.37:1025-1030
<i>Shigella dysenteriae</i>	2	23351-B1	The American Type Culture Collection
	P2	11456b	
	φ80	11456a-B1	
<i>Shigella flexeneri</i>	D20	12661-B1	The American Type Culture Collection
	SfII**		Mol.Microbiol.1997.26:939-950
	SfV**		Gene 1997.22:217-227
	Sf6**		Mol.Microbiol.1995.18:201-208
	SfX		Gene 1993.129:99-101
<i>Shigella sonnei</i>	C16**		
	Ufa		Mol..Biol (Mosk) 1977.11:323-331
<i>Shigella sp</i>	37	23354-B1	The American Type Culture Collection
<i>Spiroplasma citri</i>	SpV1		Plasmid 1993.29:193-205
<i>Spiroplasma sp.</i>	SpV1-R8A2B		Nucleic Acids Res. 1990.18:1293
	SpV3		Isr.J.Med.Sci.1987.23:429-433
	Sp V4		J.Bacteriol.1987.169:4950-4961
<i>Staphylococcus albus</i>	1 to 18, 20, 21 to 25, 27, 29 to 36 & 39		Staphylococci & Staphylococcal Infections.1997. Vol1:503-508 (Karger,Basel)

<i>Staphylococcus aureus</i>	3A	27702-B1	The American Type Culture Collection
	3C	27703-B1	
	6	27704-B1	
	15	23360-B1	
	17	23361-B1	
	29	27705-B1	
	42D**	27712-B1	
	42E	27690-B1	
	47	27691-B1	
	52	27692-B1	
	52A	27693-B1	
	53	27694-B1	
	54	27695-B1	
	55	27696-B1	
	71	27697-B1	
	75	27698-B1	
	77	27699-B1	
	79	27693-B2	
	80	27700-B1	
	81	27701-B1	
	83A	27706-B1	
	84	27707-B1	
	85**	27708-B1	
	88	33742	
	92	33741-B1	
	5504'	15565	
	K	19685-B1	
	P1	11987-B1	
	P14	11988-B1	
	UC18	15752-B1	
	44AHJD	HER 101	Felix d'Herelle Reference Centre, Quebec, Quebec
	187	HER 239	
	2638A/2854	HER 283	
	p68	HER 49	
	Twort**	HER 48	
	φ11**		J.Bacteriol.1988.170:2409-2411
	φ13** & φ42**		J.Gen..Microbiol.1989.135:1679-1697
	L54a**		J.Bacteriol.1986.166:385-391
	80α**		Can.J.Microbiol.1996.43:612-616
	94,95 & 96		J.Clin.Microbiol.1988.26:2395-2401
	φ131,A <sub>3</sub> & A <sub>5</sub>		Staphylococci & Staphylococcal Infections.1997. Vol1:503-508 (Karger,Basel)
	Phi PVL**		Gene 1998.215:57-67
<i>Staphylococcus carnosus</i>	BaSTC2		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Staphylococcus epidermidis</i>	1a, 2b, 3a, 4b, 5a, 6b, 7b, 8c, 9a, 10a, 11b,12a & 13b		Can.J.Microbiol.1988.34:1358-1361
SD-63311.4			

	41, 63, 118II, 138, 245, 336, 392 & 550		Res.Virol.1994.145:111-121
<i>Staphylococcus saprophyticus</i>	1154A, 1405, 1314, 1139 & 1259		Res.Virol.1990.141: 625-635 & Res.Virol.1994.145:111-121
<i>Staphylococcus sp.</i>	Phi 812, Phi 131, SK311 & U16		Virology 1998.246:241-252
<i>Streptococcus faecalis</i>	VD13	HER44	Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Streptococcus faecium</i>	PE1		Zentralbl.Bakteriol.1975.231:421-425
<i>Streptococcus oralis</i>	Cp-1** & Cp- 7**		FEMS Microbiol.Lett.1989.65:187-192
<i>Streptococcus pneumoniae</i>	Cp-1**	HER223	Felix d'Herelle Reference Centre, Quebec, Quebec
	Cp-1**, Cp-5**, Cp-7**, Cp-9**, ω-1 & ω-2		J.Virol.1981.40:551-559 & Eur.J.Biochem.1979.101:59-64 & Microbial Drug Resistance 1997.3:165-176
	HB-623 & HB- 746		J.Virol.1990.64:5149-5155
	EJ -1**		J.Bacteriol.1992.174:5516-5525
	Dp-2 & Dp-4		J.Virol.1978.26:221-225
	Dp-1		Virology 1975.63:577-582
	ω-3 & ω-8		J.Virol.1976.19:659-667
	304		J.Bacteriol.1980.141:1298-1304
	HB-1, HB-2, HB-3**, HB-4, HB-5 & HB-6		J.Bacteriol.1979.138:618-624
<i>Streptococcus pyogenes</i>	T12**		Mol. Microbiology. 1997#23:719-728
	A-1 A-6 A-25 Kjem	12202-B1 12203-B1 12204-B1 14918	The American Type Culture Collection
	1 182 VD1884	HER 339 HER 80 HER 323	Felix d'Herelle Refrence Centre, Quebec, Quebec
	1A 1B NN 42 118 120	12169-B1 12170-B1 21597-B1 19948-B1 19951-B2 19952-B1	The American Type Culture Collection
<i>Veillonella rodentium</i>	N2		Antonie Van Leeuwenhoek 1989.56:263-271
<i>Vibrio cholerae</i>	Psi 92		Intervirology 1993.36:237-244
	VCB-1,2,3 & 4		J.Infection 1998.36:131
	CP-T1**		J.Virol.1984.51:163-169
	VSK		FEMS Microbiol.Lett.1996.145:17-22
	Phi138		J.Virol.1986.57:960-967
	Phi149		J.Virol.1985.140:217-223



	Fs-2**		Microbiology 1998.144:1901-1906
	e4 e5 X29 $\beta$ $\kappa$ 13 14 16 24 32 57		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Vibrio cholerae</i> (Cont'd)	138 145 149 163 N-4 S-5 S-20 M-4 D-10 I II III IV V	14100-B1 14100-B2 14100-B30 14100-B4 51352-B1 51352-B2 51352-B3 51352-B4 51352-B5 51352-b6 51352-B7 51352-B8 51352-B9 51352-B10	The American Type Culture Collection
<i>Vibrio costicola</i>	UTAK		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Vibrio eltor</i>	e <sub>4</sub>		J.Gen.Virol.1987.68:1411-1416
<i>Vibrio natrigens</i>	nt1,nt6		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Vibrio</i> <i>parahaemolyticus</i>	KVP40** VF33 VP1 $\phi$ 60 $\phi$ HAWI-5 $\phi$ PEL8C-1		Felix d'Herelle Reference Centre, Quebec, Quebec
<i>Vibrio sp.</i>	$\alpha$ 3a		Felix d'Herelle Reference Centre, Quebec, Quebec
	NN ph1	11985-B1 51582-B1	The American Type Culture Collection
	Phi149		J.Virol.1987.61:3999-4006
<i>Veillonella rodentium</i>	N2		Antonie V.Leeuwenhoek.1989.56:263-271

<i>Yersinia enterocolitica</i>	1 2 3 4 5 6 7 8 9 φYeO3-12		Felix d'Herelle Reference Centre, Quebec, Quebec
	I, IV & VIII		Zentralbl. Bakteri. Mikrobiol. Hyg. 1982. 253: 102
<i>Yersinia pestis</i>	R S Y	23208-B1 11593-B1 23053-B1	The American Type Culture Collection
	II		Zh. Mikrobiol. Epidemiol. Immunobiol. 1990. 11: 9
<i>Yersinia pseudotuberculosis</i>	PST**	23207-B1	The American Type Culture Collection
<i>Yersinia sp.</i>	RD2		Mol. Gen. Mikrobiol. Virusol. 1990. 8: 18-21

Table 2

&gt;Bacteriophage 77, complete genome sequence, 41708 nucleotides

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1      gatcaaaata cttggggaac gggttagggag taaacttcgc gataatttta aaaatttcag
61     tataaccccc ctcttataac ctttttaagg caggtgatga aatggagatt atagtcgatg
121    aaaatttagt gcttaaagaa aaagaaaggc tacaagtatt atataaagac atacctagca
181    ataaattaaa agtagttgat gggttaatta ttcaagcagc aaggctacgt gtaatgcttg
241    attacatgtg ggaagacata aaagaaaaag gtgattatga tttatttact caatctgaaa
301    aggcgccacc atatgaaagg gaaagaccag tagccaaact atttaatgct agagatgctg
361    catatcaaaa aataatcaaa caattatcgg atttattgcc cgaagagaaa gaagacacag
421    aaacgccatc tgatgattac ctatgattag taataaatac gttgatgaat atataaattt
481    gtggaaacaa ggaaagataa ttttaataaa agaaaagaatt gatctcttta attatctaca
541    aaaacatata tattcacgag atgatgtata ttttgatgaa cagaaaatcg aggattgtat
601    caaattttatt gaaaaatggg attttccaac attaccattt caaaggttta tcatagctaa
661    tatattttctt atagataaaa atacagatga agctttcttt acagaatttg ctattttcat
721    gggacgtgga ggccgggaaaa acggtctaatt aagtgcattt agtgattttc tttctacgcc
781    cttacacgga gttaaagaat atcacatctc cattgttgct aatagtgaag atcaagcaaa
841    aacatcgttt gatgaaatca gaaccgtttt aatggataac aaacgaaata agacgggtta
901    aacgccaaaa gctccttatg aagtgtatta agcaaaaata ataaaccgtg caactaaatc
961    gggttattcga tataacacat caaacacaaa aaccaaaagc ggtggacgtg aggggtgtgt
1021   tatttttgat gaaattcatt atttctttgg tcctgaaatg gtaaacgtca aacgtgggtg
1081   attaggtaaa aagaaaaata gaagaacgtt ttatataagt actgatgggt ttgttagaga
1141   gggttatatt gatgcaatga agcacaaaat tgcaagtgtt ttaagtggca aggttaaaaa
1201   tagtagattg tttgcttttt attgtaagtt agacgatcca aaagaagttg atgacagaca
1261   gacgtgggaa aaggcgaacc caatgtttaca taaaccgtta tcagaatacg ctaaaacact
1321   gctaagcacg attgaagaag aatataacga tttaccattc aaccgttcaa ataagcccga
1381   attcatgact aagcgaatga atttgcctga agttgacctt gaaaaagtaa tagcaccatg
1441   gaaagaaata ctagcgacta atagagagat accaaattta gataatcaaa tgtgtattgg
1501   tggtttagac tttgcaaaaca ttcgagattt tgcaagtgtt gggctattat tccgaaaaaa
1561   cgatgattac atttgggttag gacattcgtt tgtaagacaa ggggtttttg atgatgtcaa
1621   attagaacct cctattaaag aatgggaaaa aatgggatta ttgaccattg tcgatgatga
1681   tgtcattgaa attgaaatga tagttgattg gtttttaaaag gctagagaaa aatatgggct
1741   tgaaaaagtc atagctgata attatagaac tgatattgta agacgtgcgt ttgaggatgc
1801   tggcataaaa cttgaagtac ttagaaatcc aaaagcaata catggattac ttgcaccacg
1861   tatcgatata atgtttgcga aacataacgt aatatatgga gacaatcctt tgatgcgttg
1921   gtttactaat aatgttgctg taaaaatcaa gccggatgga aataaagagt atatcaaaaa
1981   agatgaagtc agacgtaaaa cggatggatt catggctttt gttcacgcat tatatagagc
2041   agacgatata gtagacaaag acatgtctaa agcgcctgat gcattaatga gtatagattt
2101   ctaatatagg aggtgagaca tgagtattct agaaaagata tttaaaacta ggaaagatat
2161   aacatatatg cttgatttag atatgataga agatctatca caacaagcgt atgtgaaacg
2221   tttagcgatt gatagttgta ttgaatttgt tgcgcgagct gtcgctcaa gtcattttta
2281   agtattggaa ggtaatatga ttcaaaagaa tgatgtttac tacaagttaa atataaaacc
2341   aaatactgac ttatcaagcg atagtttttg gcaacaagtt atataaaac taatttatga
2401   taacgagggt ttaatcgtag taagtacag caaagaatta cttatcgcag atagctttta
2461   cagagaagag tacgctttgt atgatgatat attcaaagat gtaacggtta aagattatatac
2521   ttatcaacgt actttcacaa tgcaagaggt catatattta aagtacaaca acaataaagt
2581   gacacacttt gtagaaagtc tattcgaaga ttacgggaaa atattcggaa gaatgatagg
2641   tgcacaatta aaaaactatc aaataagagg gattttgaaa tctgcctcta gcgcatatga
2701   cgaaaagaat atagaaaaat tacaagcgtt cacaataaaa ttattcaata cttttaataa
2761   aaatcaacta gcaatcgcgc ctttgataga aggttttgat tatgaggaat tatctaattg
2821   tggtagaagt agtaacatgc ctttttctga attgagtga ctaatgagag atgcaataaa
2881   aaatgttgcg ttgatgttg gtatacctcc aggtttgatt tacggagaaa cagctgattt
2941   ggaaaaaaac acgcttgat ttgagaagtt ctgtttaaca cttttattaa aaaagattca
3001   gaacgaatta aacgcgaaac tcataacaca aagcatgtat ttgaaagata caagaataga
3061   aattgtcggg gtgaataaaa aagaccact tcaatatgct gaagcaattg acaaaactgt
3121   aagttctggt tcatttacaa ggaatgaggt gcggtattat ttaggtgaag aaccatcaga
3181   caatcctgaa ttagacgaat acctgattac taaaaactac gaaaaagcta acagtgggtg
3241   aaatgatgaa aaagaaaaag atgaaaacac tttgaaaggt ggtgatgaag atgaaagcg
3301   agattaaagg cgctaatcgtt tccaacgaag ataaatgggt ttacgaaatg cttggtatgg
3361   attcgacttg tcctaaagat gttttaacac aactagaatt tagtgatgaa gatgttgata
3421   ttataattaa ctcaaaggt ggtaacctag tagctggtag tgaaatatat acacatttaa
3481   gagctcataa aggcгааagtg aatgttcgta tcacagcaat agcagcaagt gcgcatcgc
3541   ttatcgcaat ggctgggtgac cacatcgaaa tgagtcgggt tgctagaatg atgattcaca

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3601 atccttcaag tattgcgcaa ggagaagtga aagatctaaa tcatgctgca gaaacattag  
 3661 aacattgttg tcaaataatg gctgaggcat atgctggttag agctggtaaa aacaaacaag  
 3721 aacttataga aatgatggct aaggaaacgt ggctaaatgc tgatgaagcc attgaacaag  
 3781 gttttgcgga tagtaaaatg tttgaaaacg acaatatgca aattgtagca agcgatacac  
 3841 aagtgttatc gaaagatgta ttaaactcgtg taacagcttt ggtaagtaaa acgccagagg  
 3901 ttaacattga tattgacgca atagcaaaata aagtaattga aaaaataaat atgaaagaaa  
 3961 aggaatcaga aatcgatggt gcagatagta aattatcagc aaatggattt tcaagattcc  
 4021 ttttttaata caaaaatagg aggtcataaa atgactataa atttatcgga aacattcgca  
 4081 aatgcgaaaa acgaatttat taatgcagta aacaacggtg aaccgcaaga aagacaaaat  
 4141 gaattgtacg gtgacatgat taaccaacta tttgaagaaa cttaaattaca agcaaaagca  
 4201 gaagctgaaa gagtttctag tttacctaaa tcagcacaaa ctttgagtgc aaaccaaga  
 4261 aatttcttta tggatatcaa taagagtgtt ggatataaag aagaaaaact tttaccagaa  
 4321 gaaacaattg atagaatcct cgaagattta acaacgaatc atccattatt agctgactta  
 4381 ggtattaaaa atgctgggtt gcgtttgaag ttcttaaaat ccgaaacttc tggcgtggct  
 4441 gtttggggta aaatctatgg tgaaattaaa ggtcaattag atgctgcgtt cagtgaagaa  
 4501 acagcaattc aaaataaaat gacagcgttt gttgttttac caaaaagattt aaatgatttt  
 4561 ggtcctgcgt ggattgaaag atttgttcgt gttcaaatcg aagaagcatt tgcagtggcg  
 4621 cttgaaactg cggttctaaa aggtactggt aaagaccaac cgattggctt aaaccgtcaa  
 4681 gtacaaaaag gtgtatcggg aactgatggt gcttatccag agaaagaaga acaaggtacg  
 4741 cttacatttg ctaatccgcg cgctacggtt aatgaattga cgcaagtgtt taaataccac  
 4801 tcaactaacg agaaaggtaa atcagtagcg gttaaaggta atgtaacaat ggttgttaat  
 4861 ccgtccgatg cttttgaggt tcaagcacag tatacacatt taaatgcaaa tggcgtatat  
 4921 gttactgctt taccatttaa tttgaatgtt attgagtcta cagttcaaga agcaggtaaag  
 4981 gttttaacgt acgttaaagg tctatatgat ggttatttag ctggtggtat taatgttcag  
 5041 aaattttaaag aaacacttgc gttagatgat atggatttat acactgcaaa acaatttgct  
 5101 tacggcгааг cgaaagataa taaagtgtct gctgtttgga aattagattt aaaaggacat  
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 5281 aggggagttg tatccagctg aagggtataa caatcctcgt gttgaattgt tgacaaatca  
 5341 aatcaaaaaa aagtacgaca aagtttatat cgtaccttta gataagctga caaaaacaga  
 5401 attattagaa ctatgcgaat cattacaaaa aaaagcgtct agttcaatgg ttaaaagtga  
 5461 aatcatcgac ttattgaatg gtgaagacaa tgacgattga tgatttgctt gtcaaattta  
 5521 aatcacttga aaagattgac cataattcag aggatgagta cttaaagcag ttgttaaaaa  
 5581 tgctcgtagc gcgtataaaa aatcagtcgc gagtttttga attagagaat ttaataggtc  
 5641 aagaattgat acttatacgc gctagatag cttatcaaga ttattagaa cacttcaacg  
 5701 acaattacag acctgaaata atagattttt cgttatctct aatggaggta tcagaagatg  
 5761 aagaaaagtgt ttaagaaacc actaaacggt taaatcgcg tgttctttt  
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 33001 taatggttac tttgcaactt tatacaacgt tgtaaggaa actatatctc atgaattttc  
 33061 gaaccttacc aactttggtt atctaaaact cgaaattatc aaagaaggta atgaagttta  
 33121 acaaaggaa atgtaccctt tgacgcaaac gtcaatacct attgacgcaa aaatcaatac  
 33181 ccctattgat aattctgtca ataccctat tgacgcaaat gtcaaagaga atattacaag  
 33241 tattaataat acaagtaata acaatataaa tagaatagat atattgtcgg gcaacccgac  
 33301 agcatcttct ataccctata aagaaattat cgattactta acaaaaaaag cgggcaagca  
 33361 ttttaaacac aatacagcta aaacaaaaga ttttattaaa gcaagatgga atcaagattt  
 33421 taggttgagg gattttaaaa aggtgatgta tatcaaaaca gctgagtggc taacacggga  
 33481 tagcgataaa taccttagac cagaaactct ttttggcagt aaatttgagg ggtacctcaa  
 33541 tcaaaaaata caaccaactg gcacggatca attggaacgc atgaagtacg acgaaagtta  
 33601 ttgggattag ggggatatta tgaaaccact attcagcgaa aagataaacg aaagcttgaa  
 33661 aaaatatcaa cctactcatg tcgaaaaagg attgaaatgt gagagatgtg gaagtgaata  
 33721 cgacttatat aagtttgctc ctactaaaa acaccggaat ggttacgagt ataaagacgg  
 33781 ttgcaaatgt gaaatctatg aggaatataa gcgaaacaag caacggaaga taaacaacat  
 33841 attcaatcaa tcaaactgta atccgtcttt aagagatgca acagtcaaaa actacaagcc  
 33901 acaaaatgaa aaacaagtac acgtaaaaca aacagcaata gagtacgtac aaggcttctc  
 33961 taaaaaagaa ccaaaatcat taatattgca aggttcatac ggaactggta aaagccacct  
 34021 agcatacgct atcgcaaaag cagtcaaaagc taaagggcat acggttgctt ttatgcacat  
 34081 accaatgttg atggatcgta tcaaacgac atacaacaaa aatgcagtag agactacaga  
 34141 cgagctagtc agattgctaa gtgatattga tttacttgta ctgatgata tgggtgtaga  
 34201 aaacacagag cacactttaa ataaactttt cagcattgtt gataacagag taggtaaaaa  
 34261 caacactctt acaactaact ttagtataaa agaactaaat caaaatatga actggcaacg  
 34321 tataaattcg agaattgaaa aaagacgaag aaaagtaaga gtaatcgag acgatttcag  
 34381 ggagcgagat gcatggtaac caaagaattt ttaaaaacta aacttgagtg ttcatagatg  
 34441 tacgctcaga aactcataga tgaggcacag ggcgatgaaa ataggttgta cgacctattt  
 34501 atccaaaaac ttgcagaacg tcatacacgc cccgctatcg tcgaatatta aggagtgtta  
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 34621 atcaagtata aagacaacgt aaatgaggtt tattcgctca caggagccca ttacgcgac  
 34681 gaaaagaaaa ttatgactga tagtgacctt aaacgattca aaggcgctca cgggcttcta  
 34741 tatgagcaag aattaggttt acaagcaacg atatttgata tttagaggtg gacgatgagt  
 34801 aaatacaacg ctaagaaagt tgagtacaaa ggaattgtat ttgatagcaa agtagagtgt  
 34861 gaatattacc aatattttaga aagtaatatg aatggcacta attatgatca tatcgaaata  
 34921 caaccgaaat tcgaattatt accaaaacta gataaacaac gaaagattga atatttgca  
 34981 gacttcgcgt tatatctcga tggcaaactg attgaagtta tcgacattaa aggtatgcca  
 35041 accgaagtag caaaacttaa agtaagatt ttacagacata aatacagaaa cataaaactc  
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 35161 attaaagcaa gacgagaacg caaaagagaa atgaagtgat ctaatgcaac aacaagcata  
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 35521 aagcttttag cgcgcttat ggcatgcacc taaaagaata tagagaaatg aaacaaatgg  
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 35641 agctacgtaa gaagaagcca catttgttta atgtacctca aaaacattca cgtgatccgt  
 35701 actgggttcga tgtcacttat aaccaaattg tcaagaaatg gagtgaagca taatgagcat

35761 aatcagtaac agaaaagtag atatgaacaa aacgcaagac aacgttaagc aacctgcgca  
 35821 ttacacatac ggcgacattg aaattataga ttttattgaa caagttacgg cacagtaccc  
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 36061 aagagatatc tgtatcagga taacgaacga gtggcacata tccatgtagt aaatggcact  
 36121 tattactttc acggtcatat cgtgccaggt tggcaagggtg tgaaaaagac atttgatata  
 36181 gcggaagagc ttgaaacata tataaagcaa agtgatttgg aatatgagga acagaagcaa  
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 36301 acctgaactt atccaatggg cttgggataa ccccaagtta tcaggtataa aaagattcta  
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 36481 aaaatcaaag ttaaaaaaga aatgagatta gatgaattaa ttaaatgggc gcgagaaaat  
 36541 ccggtatctat cacaaggaaa aatatttttt tcaacaggat ttagtgatgg attcgttcgt  
 36601 tttcatccaa atacaaataa gtgttcgacg tcaagtttta ttccaattga tatcccttc  
 36661 atagttgata ttgaaaaaga agtaacggaa gagactaagg ttgatagggt gattgaatta  
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 36781 tgttttatatg gcagatgtgt gcctaccaaa gcattctaca tcttaacga tgacctaac  
 36841 atgacgttaa tctggaaaaga tggggagtgt ctagtatgat gttgaaattt aaagcttggg  
 36901 ataaagataa aaaagttatg agtattattg acgaaatcga ttttaatagt gggtagattt  
 36961 tgatttcaac aggtttataa agtttcaatg aagtaaaact attacaatac acaggattta  
 37021 aagatgtgca cgggtgtggag atttatgaag gggatattgt tcaagattgt tattcgagag  
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 37321 caagaagcaa cgagatgagc ttattgggga tatagcgaag ttacgagatt gtaacaaaga  
 37381 tctagagaag aaagcaagcg catgggtag gtattgcaag agcgttgaaa aagatttaat  
 37441 aaacgaattc ggtaacgatg atgaaagagt taaattcgga atggaattaa acaataaaat  
 37501 ttttatggag gatgacacaa atgaataatc gcgaaaaaat cgaacagtcg gttattagt  
 37561 ctagtgcgta taacggtaat gacacagggg ggttgctaaa agagattgag gacgtgtata  
 37621 agaaagcgca agcgtttgat gaaatacttg agggaaatgac aaatgctatt caacattcag  
 37681 ttaagaagg tattgaactt gatgaagcag tagggattat ggcaggtcaa gttgtctata  
 37741 aatatgagga ggaataggaa aatgactaac acattacaag taaaactatt atcaaaaaat  
 37801 gctagaatgc ccgaacgaaa tcataagacg gatgcaggtt atgacatatt ctcagctgaa  
 37861 actgtcgtac tcgaaccaca agaaaaagca gtgatcaaaa cagatgtagc tgtgagtata  
 37921 ccagagggtc atgtcggact attaactagt cgtagtgggt taagtagtaa aacgtattta  
 37981 gtgattgaaa caggcaagat agacgcggga tatcatggca atttagggat taatatcaag  
 38041 aatgatgaag aacgtgatgg aatacccttt ttatatgatg atatagacgc tgaattagaa  
 38101 gatggattaa taagcatttt agatataaaa ggtaactatg tacaagatgg aagaggcata  
 38161 agaagagttt accaaatcaa caaaggcgat aaactagctc aattggttat cgtgcctata  
 38221 tggacaccgg aactaaagca agtggaggaa ttcgaaagtg tttcagaacg tggagcaaaa  
 38281 ggcttcggaa gtagcggagt gtaaagacat cttagatcga gtttaaggagg ttttggggaa  
 38341 gtgacgcaat acttagtcac aacattcaaa gattcaacag gacgaccaca tgaacattat  
 38401 actgtggcta gagataatca gacgtttaca gttattgagg cagagagtaa agaagaagcg  
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 38521 gaaaatataa gggagtgtgg gaaatgacgg atgttaaaat taaaactatt tcaggtggag  
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 38701 ttgaatcaat cacacttatt gaggagcatg ggaaatgaat cagctgagaa ttttattaca  
 38761 tgacggttagt agtttgatat tacatgaaga tgaattattt aacgaaatag tatttgtttt  
 38821 ggacaatttt agaaatgatg atgactattt aacgatagaa aaagattatg gcagagaact  
 38881 tgtattgaac aaagggttata tagttgggat caatgttgag gaggcagatg atgattaaca  
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 39181 atggatgggt tcgacatctt tattgttggg atactgtcat tattcgggtat attcgcattg  
 39241 ctacttggtt tcacattgcc tatctataca gtggctagtt accaacacaa agaattacat  
 39301 caaggaacta ttacagataa atataacaag agacaagata aagaagacaa gttctatatt  
 39361 gtattagaca acaacaagt cattgaaaat tccgacttat tattcaaaaa gaaatttgat  
 39421 agcgcagata tacaagctag gttaaaagta ggcgataagg tagaagttaa aacaatcggg  
 39481 tatagaatac acttttttaa tttatatccg gtcttatacg aagtaaagaa ggtagataaa  
 39541 caatgattaa acaaatacta agactattat tcttactagc aatgtatgag ttaggttaag  
 39601 atgtaactga gcaagtgtat attatgatga cggctaatag tgatgtagag gcgccgagtg  
 39661 attacgtctt tcgagcggag gtgagtgaat aatgagaata tttatttatg atttgatcgt  
 39721 tttgctgttt gctttcttaa tatccatata tattattgat gatggagtga taataaatgc

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39781 attaggaatt tttggatgt ataaaattat agattccttt tcagaaaata ttataaagag
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39901 gctttattca gttaaagaga tttttaggta ttttacagat tctaacttac aacgtaaaaa
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40021 gattggagct tatattattc caacagaaca gcatgaattt ttagattttt ttgatattga
40081 agtctttaat aatttagata agcaaagtaa aaaagcgtat gaaaatgtta ttggatttag
40141 acaaatgatt aatttatcaa atagagttaa ggcaatggaa gattttaaga tgagtttcaa
40201 caatgaattt agtacaaatc agattttttt taatccttct tttgttatgg aaacaattgc
40261 tattataaat gaatatcaaa aagatatatc ttatttaaaa aatataatta ataaaatgaa
40321 tgaaaataga gcttataatc atattgatag ttttatcact tcagagtacc gacgaaaaat
40381 aaacgattat aatctttatc ttgataaatt tgaagaacag tttagtcaaa agtttaaaat
40441 aaacagaact tcgataaaag aaagaattat tattaattta aacaagagga gatttaaatg
40501 atgtggatta ctatgactat tgtatttgc t atattgctat tagtttgtat cagtattaat
40561 agtgatcgtg caagagagat acaagcactt agatatatga atgattatct acttgatgaa
40621 gtagttaaaa ctaaaagggt caacgggtta gaagaataga ggattgaatt gaagcgaatg
40681 aataacgata ttaaaaagta atttatatta tcggaggtat tgcattgaat gataaagatt
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41041 gaatgggaag atatagcaca ttactttggg acaagtaaga caagtatatt acgtagaagg
41101 aatgcactga tcgataagtt agcaaagtat attggttatg tgtagcggac tttacccta
41161 tgtaagtcg cattaaaaca gtttattatg ttagtatcag attaatattt aaagttatta
41221 aatgctaata cgacgcatga acaagaggcg catcactatg tgatgtgtct tttatttat
41281 gaggtatgaa catgttcaaa ctaattgtaa atacattact acacatcaag tatagatgag
41341 tcttgatact acttaagtta tataagggtga aacattatga tgactaaaga cgaacgtata
41401 cgattctata agtctaaaga atggcaaata acaagaaaaa gagtgtctaga aagagataat
41461 tatgaatgtc aacaatgtaa gagagacggc aagttaacga catatgacaa aagcaagcgt
41521 aagtcgttgg atgtagatca tatattatcg ctagaacatc atccggagtt tgctcatgac
41581 ttaacaatt tagaaacact gtgtattaaa tgtcacaaca aaaaagaaaa gagatttata
41641 aaaaaagaaa ataaatggaa agacgaaaaa tggtaaatac ccccggtca aaaaaatcaa
41701 aagcgatc

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Table 3

	Name	Position		Name	Position
1	77ORF005	19572..21026	48	77ORF052	1762..2013
2	77ORF006	3976..5196	49	77ORF053	37521..37757
3	77ORF007	21871..23076	50	77ORF054	22818..23060
4	77ORF008	2120..3307	51	77ORF055	17546..17788
5	77ORF009	31946..32803	52	77ORF058	18892..19122
6	77ORF010	26092..26889	53	77ORF059	34564..34785
7	77ORF011	24441..25208	54	77ORF064	29574..29795
8	77ORF012	29788..30576	55	77ORF065	28528..28746
9	77ORF013	33620..34399	56	77ORF066	27494..27703
10	77ORF014	27760..28512	57	77ORF069	38341..38547
11	77ORF015	3291..4028	58	77ORF070	36269..36475
12	77ORF016	32867..33610	59	77ORF071	40498..40701
13	77ORF017	23269..23982	60	77ORF072	38735..38938
14	77ORF018	31169..31840	61	77ORF073	30945..31148
15	77ORF019	39851..40501	62	77ORF074	38544..38738
16	77ORF020	6926..7570	63	77ORF075	13673..13870
17	77ORF021	37762..38304	64	77ORF077	25357..25605
18	77ORF022	30605..31156	65	77ORF079	29089..29280
19	77ORF023	26903..27346	66	77ORF080	35204..35389
20	77ORF024	10700..11140	67	77ORF085	24060..24242
21	77ORF025	9707..10147	68	77ORF092	39706..39876
22	77ORF026	40729..41145	69	77ORF094	32226..32393
23	77ORF027	6518..6925	70	77ORF096	13606..13773
24	77ORF028	34795..35199	71	77ORF098	7092..7256
25	77ORF029	6117..6521	72	77ORF102	29051..29212
26	77ORF030	36478..36879	73	77ORF104	34393..34551
27	77ORF031	39151..39546	74	77ORF109	18282..18434
28	77ORF032	33892..34266	75	77ORF112	39543..39692
29	77ORF033	5758..6120	76	77ORF117	27361..27501
30	77ORF034	7886..8236	77	77ORF118	38390..38530
31	77ORF035	19258..19560	78	77ORF120	36059..36199
32	77ORF036	36876..37223	79	77ORF124	33699..33833
33	77ORF037	102..446	80	77ORF128	14221..14355
34	77ORF038	34908..35219	81	77ORF130	15675..15806
35	77ORF039	37220..37528	82	77ORF133	8414..8542
36	77ORF040	41377..41676	83	77ORF140	13113..13235
37	77ORF041	35454..35753	84	77ORF147	7029..7148
38	77ORF042	5490..5774	85	77ORF149	30668..30787
39	77ORF043	29304..29564	86	77ORF151	31837..31953
40	77ORF044	18481..18768	87	77ORF155	30278..30391
41	77ORF045	5216..5500	88	77ORF157	4044..4157
42	77ORF046	25663..25935	89	77ORF167	20692..20799
43	77ORF047	11159..11425	90	77ORF175	35717..35821
44	77ORF048	28776..29039	91	77ORF176	6836..6940
45	77ORF049	36013..36255	92	77ORF178	35390..35491
46	77ORF050	35753..36007	93	77ORF179	8318..8419
47	77ORF051	38931..39167	94	77ORF182	29268..29564

Table 4

## 77ORF017 sequence

23982 atgacgcataatatagaaaaacgcattaataaattaaaaacttct  
 1 M T H N I E K R I N K L K T S  
 23937 ggaaatccaaaatttataaaagtttagattcagatattcactattta  
 16 G N P K F K K L D S D I H Y L  
 23892 ctcaagagatttgaagggtgaaaaaaaccataaagggtttttatcca  
 31 L K R F E G E K N H K G F Y P  
 23847 aagtttaacaaggagaaatagttttttagatttcggtataaac  
 46 K F K Q G E I V F V D F G I N  
 23802 gttataaagaatttttctaattcacactttgcaatagtgatgaat  
 61 V N K E F S N S H F A I V M N  
 23757 aaaaatgatttctaatacggaggatatagtaaatgttattccctta  
 76 K N D S N T E D I V N V I P L  
 23712 tcctctaagaaaaacaaaaagtttttaagatgaattttgatttg  
 91 S S K E N K K Y L K M N F D L  
 23667 aaatgggagtattatttaagattgttttttaatttaattagcgcg  
 106 K W E Y Y L R L F L N L I S A  
 23622 caaaataattcagctatattaaaagaagttttcgataaaaaaac  
 121 Q N N S A I L K E V F D K K Y  
 23577 caaaaaaacaacacagaattcatcactaaagattattttattgaa  
 136 Q K N N T E F I T K D Y F I E  
 23532 tttatatctgatagtttagaaattgaaaataaattaaataaaatt  
 151 F I S D S L E I E N K L N K I  
 23487 gacagaaacattaataacatagtatcagcaattgataaggtaaaa  
 166 D R N I N N I V S A I D K V K  
 23442 aaattaaaaggtaatagttacgcttgcataaattctttccagccg  
 181 K L K G N S Y A C I N S F Q P  
 23397 attagtaagtttcgcataagaaaagttttaccccaaaaaattaaa  
 196 I S K F R I R K V L P Q K I K  
 23352 aatccagtaatagattcttcggatattatgttactgataaataga  
 211 N P V I D S S D I M L L I N R  
 23307 attaataataatatattgcagatccctgatataagatga 23269  
 226 I N N N I L Q I P D I R \*

## Physico-chemical parameters of ORF 77ORF017

1 MTHNIEKRIN KLKTSGNPKF KKLDSDIHYL LKRFEGEKNH KGFYPKFKQG  
EIVFVDFGIN  
61 VNKEFSNSHF AIVMNKNSN TEDIVNVIPL SSKENKKYLK MNFDLKWEYY  
LRLFLNLISA  
121 QNNSAILKEV FDKKYQKNNT EFITKDYFIE FISDSLEIEN KLNKIDRNIN  
NIVSAIDKVK  
181 KLKGNSYACI NSFQPISKFR IRKVLPQKIK NPVIDSSDIM LLINRINNNI LQIPDIR

**Number of amino acids:** 237

**Average molecular weight (Daltons):** 278

87.38

**Mean amino acid weight (Daltons):** 117.

67

**Monoisotopic molecular weight (Daltons):** 278

69.83

**Mean amino acid monoisotopic weight (Daltons):** 117.

59

### Amino acid composition

Aci d	Symbo l	Numb er	%	Average % in Swissprot	Aci d	Symbo l	Numb er	%	Average % in Swissprot
Ala	A	5	2.11%	7.58%	Cys	C	1	0.42%	1.66%
Asp	D	14	5.91%	5.28%	Glu	E	13	5.49%	6.37%
Phe	F	16	6.75%	4.09%	Gly	G	6	2.53%	6.84%
His	H	4	1.69%	2.24%	Ile	I	29	12.24%	5.81%
Lys	K	33	13.92%	5.95%	Leu	L	19	8.02%	9.42%
Met	M	4	1.69%	2.37%	Asn	N	30	12.66%	4.45%
Pro	P	7	2.95%	4.9%	Gln	Q	6	2.53%	3.97%
Arg	R	8	3.38%	5.16%	Ser	S	17	7.17%	7.12%
Thr	T	5	2.11%	5.67%	Val	V	11	4.64%	6.58%
Trp	W	1	0.42%	1.23%	Tyr	Y	8	3.38%	3.18%

**Number of acidic (negative) amino acids (ED):** 27  
11.39%

**Number of basic (positive) amino acids (KR):** 41  
17.30%

**Total charge (KRED):** 68  
28.69%



<b>Net charge (KR - ED):</b>	14
	5.91%
<b>Theoretical pI:</b>	10.01
<b>Total linear charge density:</b>	0.30
<b>Average hydrophobicity:</b>	-5.37
<b>Ratio of hydrophilicity to hydrophobicity:</b>	1.41
<b>Percentage of hydrophilic amino acid:</b>	57.81%
<b>Percentage of hydrophobic amino acid:</b>	42.19%
<b>Ratio of %hydrophilic to %hydrophobic:</b>	1.37

SD-63311.4

**77ORF019 sequence**

```

39851      atgaacgagcaaataataggaagcatatatacttttagcaggaggt
1      M  N  E  Q  I  I  G  S  I  Y  T  L  A  G  G
39896      gttgtgctttattcagttaaagagatttttaggtattttacagat
16     V  V  L  Y  S  V  K  E  I  F  R  Y  F  T  D
39941      tctaacttacaaacgtaaaaaaatcaatttagaacaatatatccg
31     S  N  L  Q  R  K  K  I  N  L  E  Q  I  Y  P
39986      atatatttagattgttttaaaaaggctaaaaagatgattggagct
46     I  Y  L  D  C  F  K  K  A  K  K  M  I  G  A
40031      tatattattccaacagaacagcatgaatttttagatttttttgat
61     Y  I  I  P  T  E  Q  H  E  F  L  D  F  F  D
40076      attgaagtctttaataatttagataagcaaagtaaaaaagcgtat
76     I  E  V  F  N  N  L  D  K  Q  S  K  K  A  Y
40121      gaaaatgttattggatttagacaaatgattaatttatcaaataga
91     E  N  V  I  G  F  R  Q  M  I  N  L  S  N  R
40166      gttaaggcaatggaagattttaagatgagtttcaacaatgaattt
106    V  K  A  M  E  D  F  K  M  S  F  N  N  E  F
40211      agtacaatatcagattttttttaatccttcttttgttatggaaaca
121    S  T  N  Q  I  F  F  N  P  S  F  V  M  E  T
40256      attgctattataaatgaatatcaaaaagatatatcttatttataaa
136    I  A  I  I  N  E  Y  Q  K  D  I  S  Y  L  K
40301      aatataattaataaaaatgaatgaaaatagagcttataatcatatt
151    N  I  I  N  K  M  N  E  N  R  A  Y  N  H  I
40346      gatagttttatcacttcagagtaccgacgaaaaataaacgattat
166    D  S  F  I  T  S  E  Y  R  R  K  I  N  D  Y
40391      aatctttatcttgataaatttgaagaacagtttagtcaaaaagttt
181    N  L  Y  L  D  K  F  E  E  Q  F  S  Q  K  F
40436      aaaataaacagaacttcgataaaaagaaagaattattattaattta
196    K  I  N  R  T  S  I  K  E  R  I  I  I  N  L
40481      aacaagaggagattttaaatga 40501
211    N  K  R  R  F  K  *

```

## Physico-chemical parameters of ORF 77ORF019

1 MNEQIIGSIY TLAGGVVLYS VKEIFRYFTD SNLQRKKINL EQIYPIYLDC  
FKKAKKMIGA  
61 YIIPTEQHEF LDFFDIEVFN NLDKQSKKAY ENVIGFRQMI NLSNRVKAME  
DFKMSFNNEF  
121 STNQIFFNPS FVMETIAIIN EYQKDISYLK NIINKMNENR AYNHIDSFIT  
SEYRRKINDY  
181 NLYLDKFEEQ FSQKFKINRT SIKERIINL NKRRFK

**Number of amino acids:** 216

**Average molecular weight (Daltons):** 260

26.06

**Mean amino acid weight (Daltons):** 120.

49

**Monoisotopic molecular weight (Daltons):** 260

09.34

**Mean amino acid monoisotopic weight (Daltons):** 120.

41

### Amino acid composition

Aci d	Symbo l	Numb er	%	Average % in Swissprot	Aci d	Symbo l	Numb er	%	Average % in Swissprot
Ala	A	7	3.24%	7.58%	Cys	C	1	0.46%	1.66%
Asp	D	10	4.63%	5.28%	Glu	E	16	7.41%	6.37%
Phe	F	19	8.80%	4.09%	Gly	G	5	2.31%	6.84%
His	H	2	0.93%	2.24%	Ile	I	28	12.96 %	5.81%
Lys	K	22	10.19 %	5.95%	Leu	L	12	5.56%	9.42%
Met	M	7	3.24%	2.37%	Asn	N	23	10.65 %	4.45%
Pro	P	3	1.39%	4.9%	Gln	Q	10	4.63%	3.97%
Arg	R	11	5.09%	5.16%	Ser	S	13	6.02%	7.12%
Thr	T	7	3.24%	5.67%	Val	V	7	3.24%	6.58%
Trp	W	0	0.00%	1.23%	Tyr	Y	13	6.02%	3.18%

**Number of acidic (negative) amino acids (ED):** 26  
12.04%

**Number of basic (positive) amino acids (KR):** 33  
15.28%

**Total charge (KRED):** 59  
27.31%

**Net charge (KR - ED):** 7  
3.24%

<b>Theoretical pI:</b>	9.52
<b>Total linear charge density:</b>	0.28
<b>Average hydrophobicity:</b>	-4.84
<b>Ratio of hydrophilicity to hydrophobicity:</b>	1.37
<b>Percentage of hydrophilic amino acid:</b>	54.17%
<b>Percentage of hydrophobic amino acid:</b>	45.83%
<b>Ratio of %hydrophilic to %hydrophobic:</b>	1.18

SD-63311.4

**77ORF043 sequence**

```
29304      atgtattacgaaataggcgaaatcatacgcaaaaatattcatggt
1      M  Y  Y  E  I  G  E  I  I  R  K  N  I  H  V
29349      aacggattcgattttaagctattcatttttaaagggtcatatgggc
16     N  G  F  D  F  K  L  F  I  L  K  G  H  M  G
29394      atatcaatacaagttaaagatatgaacaacgtaccaattaaacat
31     I  S  I  Q  V  K  D  M  N  N  V  P  I  K  H
29439      gcttatgtcgtagatgagaatgacttagatatggcatcagactta
46     A  Y  V  V  D  E  N  D  L  D  M  A  S  D  L
29484      tttaaccaagcaatagatgaatggattgaagagaacacagacgaa
61     F  N  Q  A  I  D  E  W  I  E  E  N  T  D  E
29529      caggacagactaattaacttagtcatgaaatggtag 29564
76     Q  D  R  L  I  N  L  V  M  K  W  *
```

662027 " 25245460

# Physico-chemical parameters of ORF 77ORF043

1 MYYEIGEIR KNIHVNGFDF KLFILKGHMG ISIQVKDMNN VPIKHAYVVD  
 ENLDLDMASDL  
 61 FNQAIDEWIE ENTDEQDRLI NLVMKW

Number of amino acids: 86  
 Average molecular weight (Daltons): 101  
 86.68  
 Mean amino acid weight (Daltons): 118.  
 45  
 Monoisotopic molecular weight (Daltons): 101  
 80.02  
 Mean amino acid monoisotopic weight (Daltons): 118.  
 37

## Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	3	3.49%	7.58%	Cys	C	0	0.00%	1.66%
Asp	D	9	10.47%	5.28%	Glu	E	7	8.14%	6.37%
Phe	F	4	4.65%	4.09%	Gly	G	4	4.65%	6.84%
His	H	3	3.49%	2.24%	Ile	I	11	12.79%	5.81%
Lys	K	6	6.98%	5.95%	Leu	L	6	6.98%	9.42%
Met	M	5	5.81%	2.37%	Asn	N	8	9.30%	4.45%
Pro	P	1	1.16%	4.9%	Gln	Q	3	3.49%	3.97%
Arg	R	2	2.33%	5.16%	Ser	S	2	2.33%	7.12%
Thr	T	1	1.16%	5.67%	Val	V	6	6.98%	6.58%
Trp	W	2	2.33%	1.23%	Tyr	Y	3	3.49%	3.18%

Number of acidic (negative) amino acids (ED): 16  
 18.60%  
 Number of basic (positive) amino acids (KR): 8  
 9.30%  
 Total charge (KRED): 24  
 27.91%  
 Net charge (KR - ED): -8  
 -9.30%  
 Theoretical pI: 4.38  
 Total linear charge density: 0.30  
 Average hydrophobicity: -2.80  
 Ratio of hydrophilicity to hydrophobicity: 1.19

<b>Percentage of hydrophilic amino acid:</b>	48.84%
<b>Percentage of hydrophobic amino acid:</b>	51.16%
<b>Ratio of %hydrophilic to %hydrophobic:</b>	0.95

662031.4 248/037

**77ORF102 sequence**

```
29051      atgagcaacattttataaaaagctacctagtagcagtattatgcttc
1      M  S  N  I  Y  K  S  Y  L  V  A  V  L  C  F
29096      acagtcttagcgattgtacttatgccgtttctatacttcactaca
16     T  V  L  A  I  V  L  M  P  F  L  Y  F  T  T
29141      gcatggtcaattgcgggattcgcaagtatcgcaacattcatgtac
31     A  W  S  I  A  G  F  A  S  I  A  T  F  M  Y
29186      tacaaagaatgcttttttcaaagaataa 29212
46     Y  K  E  C  F  F  K  E  *
```

SD-63311.4



## Physico-chemical parameters of ORF 77ORF102

1 MSNIYKSYLV AVLCTVLAI VLMPFLYFTT AWSIAGFASI ATFMYYKECF FKE

Number of amino acids: 53

Average molecular weight (Daltons): 61

55.42

Mean amino acid weight (Daltons): 11

6.14

Monoisotopic molecular weight (Daltons): 61

51.07

Mean amino acid monoisotopic weight (Daltons): 11

6.06

### Amino acid composition

Aci d	Symbo l	Numb er	%	Average % in Swissprot	Aci d	Symbo l	Numb er	%	Average % in Swissprot
Ala	A	6	11.32 %	7.58%	Cys	C	2	3.77 %	1.66%
Asp	D	0	0.00%	5.28%	Glu	E	2	3.77 %	6.37%
Phe	F	7	13.21 %	4.09%	Gly	G	1	1.89 %	6.84%
His	H	0	0.00%	2.24%	Ile	I	4	7.55 %	5.81%
Lys	K	3	5.66%	5.95%	Leu	L	5	9.43 %	9.42%
Met	M	3	5.66%	2.37%	Asn	N	1	1.89 %	4.45%
Pro	P	1	1.89%	4.9%	Gln	Q	0	0.00 %	3.97%
Arg	R	0	0.00%	5.16%	Ser	S	4	7.55 %	7.12%
Thr	T	4	7.55%	5.67%	Val	V	4	7.55 %	6.58%
Trp	W	1	1.89%	1.23%	Tyr	Y	5	9.43 %	3.18%

Number of acidic (negative) amino acids (ED): 2 3.77%

Number of basic (positive) amino acids (KR): 3 5.66%

Total charge (KRED): 5 9.43%

Net charge (KR - ED): 1 1.89%

Theoretical pI: 8.18

Total linear charge density: 0.13

<b>Average hydrophobicity:</b>	10.81
<b>Ratio of hydrophilicity to hydrophobicity:</b>	0.40
<b>Percentage of hydrophilic amino acid:</b>	28.30%
<b>Percentage of hydrophobic amino acid:</b>	71.70%
<b>Ratio of %hydrophilic to %hydrophobic:</b>	0.39

662027 232450

**77ORF104 sequence**

```
34393      atggtaaccaaagaattttttaaaaactaaacttgagtgttcagat
1      M  V  T  K  E  F  L  K  T  K  L  E  C  S  D
34438      atgtacgctcagaaactcatagatgaggcacagggcgatgaaaat
16     M  Y  A  Q  K  L  I  D  E  A  Q  G  D  E  N
34483      aggttggtacgacctatttatccaaaaacttgcagaacgtcataca
31     R  L  Y  D  L  F  I  Q  K  L  A  E  R  H  T
34528      cgccccgctatcgtcgaatattaa 34551
46     R  P  A  I  V  E  Y  *
```

SD-63311.4

# Physico-chemical parameters of ORF 77ORF104

1 MVTKEFLKTK LECSDMYAQK LIDEAQGDEN RLYDLFIQKL AERHTRPAIV EY

Number of amino acids: 52

Average molecular weight (Daltons): 61

93.13

Mean amino acid weight (Daltons): 11

9.10

Monoisotopic molecular weight (Daltons): 61

89.12

Mean amino acid monoisotopic weight (Daltons): 11

9.02

## Amino acid composition

Aci d	Symbo l	Numb er	%	Average % in Swissprot	Aci d	Symbo l	Numb er	%	Average % in Swissprot
Ala	A	4	7.69 %	7.58%	Cys	C	1	1.92%	1.66%
Asp	D	4	7.69 %	5.28%	Glu	E	6	11.54 %	6.37%
Phe	F	2	3.85 %	4.09%	Gly	G	1	1.92%	6.84%
His	H	1	1.92 %	2.24%	Ile	I	3	5.77%	5.81%
Lys	K	5	9.62 %	5.95%	Leu	L	6	11.54 %	9.42%
Met	M	2	3.85 %	2.37%	Asn	N	1	1.92%	4.45%
Pro	P	1	1.92 %	4.9%	Gln	Q	3	5.77%	3.97%
Arg	R	3	5.77 %	5.16%	Ser	S	1	1.92%	7.12%
Thr	T	3	5.77 %	5.67%	Val	V	2	3.85%	6.58%
Trp	W	0	0.00 %	1.23%	Tyr	Y	3	5.77%	3.18%

Number of acidic (negative) amino acids (ED): 10  
19.23%

Number of basic (positive) amino acids (KR): 8  
15.38%

Total charge (KRED): 18  
34.62%

<b>Net charge (KR - ED):</b>	-2
	-3.85%
<b>Theoretical pI:</b>	5.03
<b>Total linear charge density:</b>	0.38
<b>Average hydrophobicity:</b>	-5.81
<b>Ratio of hydrophilicity to hydrophobicity:</b>	1.47
<b>Percentage of hydrophilic amino acid:</b>	53.85%
<b>Percentage of hydrophobic amino acid:</b>	46.15%
<b>Ratio of %hydrophilic to %hydrophobic:</b>	1.17

SD-63311.4

**77ORF182 sequence**

```
29268      atgttcaatataaaaacgaaaaacggaggaagtcaagatgtattac
1      M  F  N  I  K  R  K  T  E  E  V  K  M  Y  Y
29313      gaaataggcgaaatcatacgcaaaaatattcatgttaacggattc
16     E  I  G  E  I  I  R  K  N  I  H  V  N  G  F
29358      gatTTtaagctatttcatttttaaagggtcatatgggcatatcaata
31     D  F  K  L  F  I  L  K  G  H  M  G  I  S  I
29403      caagttaaagatatgaacaacgtaccaattaaacatgcttatgtc
46     Q  V  K  D  M  N  N  V  P  I  K  H  A  Y  V
29448      gtagatgagaatgacttagatatggcatcagacttatttaaccaa
61     V  D  E  N  D  L  D  M  A  S  D  L  F  N  Q
29493      gcaatagatgaatggattgaagagaacacagacgaacaggacaga
76     A  I  D  E  W  I  E  E  N  T  D  E  Q  D  R
29538      ctaattaacttagtcatgaaatggtag 29564
91     L  I  N  L  V  M  K  W  *
```

# Physico-chemical parameters of ORF 77ORF182

1 MFNIKRKTEE VKMYEIGEI IRKNIHVNGF DFKLFILKGH MGISIQVKDM  
 NNVPIKHAYV  
 61 VDENDLDMAS DLFNQAIWEV IEENTDEQDR LINLVMKW

Number of amino acids: 98  
 Average molecular weight (Daltons): 116  
 91.50  
 Mean amino acid weight (Daltons): 119.  
 30  
 Monoisotopic molecular weight (Daltons): 116  
 83.84  
 Mean amino acid monoisotopic weight (Daltons): 119.  
 22

## Amino acid composition

Aci d	Symbo l	Numb er	%	Average % in Swissprot	Aci d	Symbo l	Numb er	%	Average % in Swissprot
Ala	A	3	3.06 %	7.58%	Cys	C	0	0.00%	1.66%
Asp	D	9	9.18 %	5.28%	Glu	E	9	9.18%	6.37%
Phe	F	5	5.10 %	4.09%	Gly	G	4	4.08%	6.84%
His	H	3	3.06 %	2.24%	Ile	I	12	12.24 %	5.81%
Lys	K	9	9.18 %	5.95%	Leu	L	6	6.12%	9.42%
Met	M	6	6.12 %	2.37%	Asn	N	9	9.18%	4.45%
Pro	P	1	1.02 %	4.9%	Gln	Q	3	3.06%	3.97%
Arg	R	3	3.06 %	5.16%	Ser	S	2	2.04%	7.12%
Thr	T	2	2.04 %	5.67%	Val	V	7	7.14%	6.58%
Trp	W	2	2.04 %	1.23%	Tyr	Y	3	3.06%	3.18%

Number of acidic (negative) amino acids (ED): 18  
 18.37%

<b>Number of basic (positive) amino acids (KR):</b>	12
	12.24%
<b>Total charge (KRED):</b>	30
	30.61%
<b>Net charge (KR - ED):</b>	-6
	-6.12%
<b>Theoretical pI:</b>	4.76
<b>Total linear charge density:</b>	0.33
<b>Average hydrophobicity:</b>	-3.89
<b>Ratio of hydrophilicity to hydrophobicity:</b>	1.28
<b>Percentage of hydrophilic amino acid:</b>	51.02%
<b>Percentage of hydrophobic amino acid:</b>	48.98%
<b>Ratio of %hydrophilic to %hydrophobic:</b>	1.04

663311.4



Table 5

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100017|lan|77ORF017 Phage 77 ORF |23269-23982|-3  
(237 letters)

Database: nr

393,678 sequences; 120,452,765 total letters

Sequences producing significant alignments:	Score	E
Value	(bits)	
gi 4493986 emb CAB39045.1  (AL034559) predicted using hexExon; ...	41	
0.010		
gi 730607 sp P23250 RPI1_YEAST NEGATIVE RAS PROTEIN REGULATOR P...	38	
0.053		
gi 3097044 emb CAA75299  (Y15035) K1R [Cowpox virus]	38	
0.090		
gi 2146245 pir S73794 hypothetical protein H91_orf180 - Mycopl...	38	
0.090		
gi 83910 pir S04682 ribosomal protein var1 - yeast (Candida gl...	37	
0.15		
gi 133135 sp P21358 RMAR_CANGA MITOCHONDRIAL RIBOSOMAL PROTEIN ...	37	
0.15		
gi 2128843 pir H64475 hypothetical protein MJ1409 - Methanococ...	36	
0.20		
gi 5107017 gb AAD39926.1 AF126285_2 (AF126285) RNA polymerase [...]	36	
0.35		
gi 2146210 pir S73342 hypothetical protein E07_orf166 - Mycopl...	35	
0.60		

Database: swissprot

79,449 sequences; 28,874,452 total letters

Sequences producing significant alignments:	Score	E
Value	(bits)	
sp P23250 RPI1_YEAST NEGATIVE RAS PROTEIN REGULATOR PROTEIN.	38	0.014
sp P21358 RMAR_CANGA MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1.	37	0.040
sp Q21444 LDLC_CAEL LDLC PROTEIN HOMOLOG.	34	0.35
sp P27240 RFAY_ECOLI LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROT.	33	0.46
sp P53192 YGC0_YEAST HYPOTHETICAL 27.1 KD PROTEIN IN ALK1-CKB1.	33	0.60
sp P32908 SMC1_YEAST CHROMOSOME SEGREGATION PROTEIN SMC1 (DA-B.	33	0.60
sp P54683 TAGB_DICDI PRESTALK-SPECIFIC PROTEIN TAGB PRECURSOR .	32	0.78
sp Q03100 CYAA_DICDI ADENYLATE CYCLASE, AGGREGATION SPECIFIC (.	32	0.78

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100019|lan|77ORF019 Phage 77 ORF|39851-40501|2  
(216 letters)

Database: nr  
373,355 sequences; 114,214,446 total letters

Sequences producing significant alignments:		Score (bits)	E Value
gi 3341966 dbj BAA31932	(AB009866) orf 59 [bacteriophage phi PVL]	437	e-122
gi 2689911	(AE000792) B. burgdorferi predicted coding region BB...	38	0.058
gi 1171589 emb CAA64574	(X95275) frameshift [Plasmodium falcip...	37	0.10
gi 4493986 emb CAB39045.1	(AL034559) predicted using hexExon; ...	36	0.23
gi 141257 sp P18019 YPI9_CLOPE	HYPOTHETICAL 14.5 KD PROTEIN (OR...	36	0.29
gi 133412 sp P27059 RPOB_ASTLO	DNA-DIRECTED RNA POLYMERASE BETA...	35	0.51
gi 3122231 sp Q58851 HISX_METJA	HISTIDINOL DEHYDROGENASE (HDH) ...	35	0.51
gi 3649757 emb CAB11106.1	(Z98547) predicted using hexExon; MA...	34	0.66
gi 2688313	(AE001146) sensory transduction histidine kinase, pu...	34	0.87

Database: swissprot  
79,449 sequences; 28,874,452 total letters

Sequences producing significant alignments:		Score (bits)	E Value
sp P18019 YPI9_CLOPE	HYPOTHETICAL 14.5 KD PROTEIN (ORF9).	36	0.079
sp Q58851 HISX_METJA	HISTIDINOL DEHYDROGENASE (EC 1.1.1.23) (H.	35	0.14
sp P27059 RPOB_ASTLO	DNA-DIRECTED RNA POLYMERASE BETA CHAIN (E.	35	0.14
sp Q02224 CENE_HUMAN	CENTROMERIC PROTEIN E (CENP-E PROTEIN).	34	0.31
sp P04931 ARP_PLAFA	ASPARAGINE-RICH PROTEIN (AG319) (ARP) (FRA..	33	0.53
sp P18011 IPAB_SHIFL	62 KD MEMBRANE ANTIGEN.	32	0.69
sp P18709 VTA2_XENLA	VITELLOGENIN A2 PRECURSOR (VTG A2) [CONTA..	32	0.90
sp Q64409 CP3H_CAVPO	CYTOCHROME P450 3A17 (EC 1.14.14.1) (CYPI..	32	0.90
sp P21358 RMAR_CANGA	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1.	32	0.90
sp Q03945 IPAB_SHIDY	62 KD MEMBRANE ANTIGEN.	32	1.2

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100043|lan|77ORF043 Phage 77 ORF|29304-29564|3  
(86 letters)

Database: nr

373,355 sequences; 114,214,446 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 3341947 dbj BAA31913  (AB009866) orf 39 [bacteriophage phi PVL]	182	6e-46
gi 744518 prf 2014422A FKBP-rapamycin-associated protein [Homo...	32	0.84
gi 1169736 sp P42346 FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN...	32	0.84
gi 1169735 sp P42345 FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIATED PROTE...	32	0.84
gi 3282239 (U88966) rapamycin associated protein FRAP2 [Homo sa...	32	0.84
gi 3875402 emb CAA98122  (Z73906) cDNA EST EMBL:D64544 comes fr...	31	2.5
gi 1084792 pir S54091 hypothetical protein YPR070w - yeast (Sa...	30	4.2

Database: swissprot

79,449 sequences; 28,874,452 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P42345 FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) .	32	0.24
sp P42346 FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (R.	32	0.24
sp P34554 YNP1_CAEEL HYPOTHETICAL 42.2 KD PROTEIN T05G5.1 IN C.	28	3.5
sp Q24118 LIO_DROME LINOTTE PROTEIN.	28	3.5
sp P80034 ACH2_BOMMO ANTICHYMOTRYPSIN II (ACHY-II).	28	3.5
sp P22922 A1AT_BOMMO ANTITRYPSIN PRECURSOR (AT).	28	3.5
sp Q44363 TRAA_AGRT6 CONJUGAL TRANSFER PROTEIN TRAA.	28	3.5
sp P38255 YBU5_YEAST HYPOTHETICAL 51.3 KD PROTEIN IN PHO5-VPS1.	27	6.0
sp P55822 SH3B_HUMAN SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PRO.	27	7.9
sp Q58482 YA82_METJA HYPOTHETICAL PROTEIN MJ1082.	27	7.9
sp P34252 YKK8_YEAST HYPOTHETICAL 52.3 KD PROTEIN IN HAP4-AAT1.	27	7.9

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100102|lan|77ORF102 Phage 77 ORF|29051-29212|2  
(53 letters)

Database: nr  
373,355 sequences; 114,214,446 total letters

	Score (bits)	E Value
Sequences producing significant alignments:		
gi 3341946 dbj BAA31912  (AB009866) orf 38 [bacteriophage phi PVL]	96	3e-20
gi 4325288 gb AAD17315  (AF123593) voltage-dependent sodium cha...	28	7.1
gi 2649684 (AE001040) A. fulgidus predicted coding region AF092...	28	9.3

Database: swissprot  
79,449 sequences; 28,874,452 total letters

	Score (bits)	E Value
Sequences producing significant alignments:		
sp P42087 HUTM_BACSU PUTATIVE HISTIDINE PERMEASE.	26	7.1
sp P04775 CIN2_RAT SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBU...	26	9.2
sp P42619 YQJF_ECOLI HYPOTHETICAL 17.2 KD PROTEIN IN EXUR-TDCC...	26	9.2

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|100104|lan|77ORF104 Phage 77 ORF|34393-34551|1  
(52 letters)

Database: nr  
373,355 sequences; 114,214,446 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 2315523 (AF016452) similar to the leucine-rich domains found...	29	4.2
gi 4377168 gb AAD18990  (AE001666) CT711 hypothetical protein [...	29	5.4
gi 3882171 dbj BAA34445  (AB018268) KIAA0725 protein [Homo sapi...	28	9.3

Database: swissprot  
79,449 sequences; 28,874,452 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P04879 RRPP_VSVIG RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48.	27	5.4
sp P04880 RRPP_VSVIM RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48.	27	5.4
sp Q13946 CN7A_HUMAN HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC .	26	7.1
sp P35381 ATPA_DROME ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL P.	26	9.3
sp P54659 MVPB_DICDI MAJOR VAULT PROTEIN BETA (MVP-BETA) .	26	9.3
sp P40397 YHXC_BACSU HYPOTHETICAL OXIDOREDUCTASE IN APRE-COMK .	26	9.3

BLASTP 2.0.8 [Jan-05-1999]

Query= sid|122748|lan|77ORF182 Phage 77 ORF|29268-29564|3  
(98 letters)

Database: nr

393,678 sequences; 120,452,765 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 3341947 dbj BAA31913.1  (AB009866) orf 39 [bacteriophage phi..	182	8e-46
gi 1084792 pir  S54091 hypothetical protein YPR070w - yeast (Sa..	35	0.13
gi 1169736 sp P42346 FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN..	32	1.1
gi 744518 prf  2014422A FKBP-rapamycin-associated protein [Homo..	32	1.1
gi 5051381 emb CAB44736.1  (AL049653) dJ647M16.2 (FK506 binding..	32	1.1
gi 4826730 ref NP_004949.1 pFRAP1  FK506 binding protein 12-rap..	32	1.1
gi 3282239 (U88966) rapamycin associated protein FRAP2 [Homo sa..	32	1.1

Database: swissprot

79,909 sequences; 29,054,478 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P42345 FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) .	32	0.29
sp P42346 FRAP_RAT FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (R.	32	0.29
sp P40557 YIA5_YEAST PUTATIVE DISULFIDE ISOMERASE YIL005W PREC.	29	3.3
sp Q24118 LIO_DROME LINOTTE PROTEIN.	28	4.4
sp Q44363 TRAA_AGR6 CONJUGAL TRANSFER PROTEIN TRAA.	28	4.4
sp P80034 ACH2_BOMMO ANTICHYMOTRYPSIN II (ACHY-II).	28	4.4
sp P34554 YNP1_CAEEL HYPOTHETICAL 42.2 KD PROTEIN T05G5.1 IN C.	28	4.4
sp P22922 A1AT_BOMMO ANTITRYPSIN PRECURSOR (AT).	28	4.4

Table 6

1st position (5' end)	2nd position				3rd position (3' end)
	U	C	A	G	
<b>U</b>	Phe	Ser	Tyr	Cys	<b>U</b>
	Phe	Ser	Tyr	Cys	<b>C</b>
	Leu	Ser	Stop	Stop	<b>A</b>
	Leu	Ser	Stop	Trp	<b>G</b>
<b>C</b>	Leu	Pro	His	Arg	<b>U</b>
	Leu	Pro	His	Arg	<b>C</b>
	Leu	Pro	Gln	Arg	<b>A</b>
	Leu	Pro	Gln	Arg	<b>G</b>
<b>A</b>	Ile	Thr	Asn	Ser	<b>U</b>
	Ile	Thr	Asn	Ser	<b>C</b>
	Ile	Thr	Lys	Arg	<b>A</b>
	Met	Thr	Lys	Arg	<b>G</b>
<b>G</b>	Val	Ala	Asp	Gly	<b>U</b>
	Val	Ala	Asp	Gly	<b>C</b>
	Val	Ala	Glu	Gly	<b>A</b>
	Val	Ala	Glu	Gly	<b>G</b>

Table 7

Bacteriophage 3A, complete genome sequence

1	caaacgctag	caacgcggat	aaatttttca	tgaaggggg	tctttatatg	aagttaacaa	aaaaacagct
71	aaaagaatat	atagaagatt	acaaaaaatc	tgatgacata	ttaattaatt	tgtatataga	aacatatgaa
141	ttttattgtc	ggttaagaga	tgaacttaaa	aatagtgtat	taatgataga	gcatacaaac	aaggctgggtg
211	cgagcaatat	tattaagaat	ccattaagca	tagaactgac	aaaaacagtt	caaacactaa	ataacttact
281	caagtctatg	ggtttaactg	cagcacaaag	aaaaaagata	gttcaagaag	aaggtggatt	cggtgactat
351	taaagtttta	aatgaacctt	cacaaaaact	attaacaaca	tggtatgcag	agcaagtcac	tcaagggaaa
421	ataaaaacaa	gcaaatatgt	tagaaaagaa	tgtgagagac	atcttagata	tctagaaaat	ggaggtaaat
491	gggtatttga	tgaagaatta	gcgcattcgt	ctattcgatt	tatagaaaag	ttttgtaaac	cttccaaagg
561	atctaaacgt	caacttgtat	tacagccatg	gcaacatttt	attatcggca	gtttgttttg	ttgggttcat
631	aaagaaccaa	aactgcgcag	gtttaaagaa	gctttgatata	ttatggggcg	aaaaaatggt	aaaacaacca
701	ctatttctgg	ggttgctaac	tatgctgtat	cacaagatgg	agaaaatggt	gcagaaattc	atttgttagc
771	aaacgtaatg	aaacaagcta	ggattctatt	tgatgaatct	aaggcgtatg	ttaaagctag	cccaaagctt
841	gataaaaaat	tcagaacatt	aagagatgaa	atccattatg	acgcaacgat	atcaaaaatt	atccccaag
911	catcagatag	cgataagtta	gatggattga	atacacacat	ggggattttt	gatgaaattc	atgaatttaa
981	agactataaaa	ttgatttcag	ttataaaaaa	ctcaagagct	gcaaggttac	aacctcttct	catctacatt
1051	acgacagcag	gggtatcaatt	agatgggtcca	cttggttgata	tggtagaagc	gggaagagac	accttagatc
1121	aatcatatga	agacgaaaga	actttttatt	atttagcatc	tttggtatgat	gacgatgata	ttaatgatct
1191	gtcgaactgg	ataaaagcaa	atcccaactt	aggtgtctct	ataaatttag	atgagatgaa	agaagagttg
1261	gaaaaagcta	agagaacacc	agctgaacgt	ggagatttta	taaccaaaag	gtttaaatatc	tttgctaata
1331	atgacgagat	gagttttatt	gattacccaa	cactccaaaa	aaataatgaa	attgtttctt	tagaagagct
1401	gggaaggcaga	ccgtgcacga	ttggttatga	tttatcagaa	acagaggact	ttacagccgc	gtgtgctact
1471	tttgcgttag	ataatggtaa	agttgcagtt	ttatcgcat	catggattcc	taagcacaaa	gttgaattat
1541	ctaaccgaaa	aataccctat	agagaatggg	aagaagatgg	cttattaaca	gtgcaagata	agccttatat
1611	tgactaccaa	gatgttttaa	attggataat	taagatgaat	gagcattatg	tagtagaaaa	aattacttat
1681	gatagagcga	acgcattcaa	actaaatcaa	gagttaaaaa	attacgggtt	tgaaacggga	gaaacaagac
1751	aaggagcttt	gaccttgagc	ctgcatttaa	aggattttaa	agaaatgttt	ttagatggga	aaataattat
1821	taataataat	ctcttaatat	aatggatgat	caataatgtt	cagttgaaac	tagacagaaa	cggaaactgg
1891	ttgcccgtcta	agcaaagcag	atatcgtaaa	atagatggct	ttgcagcatt	tttaaacaca	tatacagata
1961	ttatgaataa	agttgtttct	gatagtggtg	aaggaaacat	agagtttatt	agtattaaag	acataatgag
2031	ttaaggagggt	gaatgttatc	gcaaaaagaga	atatgttcac	acgcataaag	aaaaaattga	tagacaattg
2101	gattgatcag	tcaacttcta	agctttatga	ctttagccca	tggaaaaata	gatctttttg	gggtgtaatt
2171	aataatacgc	ttgaaactaa	tgaacgata	ttttcagcta	ttacaaagtt	atctaattcg	atggctagt
2241	tgcccttgaa	aatgtatgaa	gattataaag	tagttataac	agaagtatct	gatttactta	cagtgctacc
2311	gaataattct	ctgagcagtt	ttgattttat	taatacaaat	gaaacaatca	gaaatgaaa	aggtaatgca
2381	tatgtctcaa	ttgaacgaga	catctatcat	caaccatcaa	agcttttctt	atataatcca	gaggtgtgtg
2451	aaatgttaat	tgaaaaccaa	tcacgtgaac	tttattattc	cattcatgct	gcaactggaa	ataaattgat
2521	tgttcataat	atggacatgt	tgcattttaa	acacatcgtg	gcattctaata	tggtgcaagg	cattagtcag
2591	attgatgtgt	tgaagaatac	aactgatttt	gataatgcag	taagaacctt	taactcttaca	gaaatgcaaa
2661	aacctgattc	tttcatgctt	aaatatggtt	ccaatgtagg	taagaacaaa	agggcagcaag	tggtagaaga
2731	tttcaaacag	tactatgaag	aaaacgggtg	aatattattc	caagagcctg	gtgttgaaat	cgaaccgtta
2801	cctaaaaaat	atgtctctga	agatatagtg	gcaagcgaga	atttaacaag	agaaagagta	gctaaccgtt
2871	ttcaattgac	ctcagtatct	ttaaatgcaa	gatcaaatat	aaatttcgag	aaaaatgaag	agttaaacag
2941	attttacttg	cagcataacct	tattgccaat	cgtcaaacag	tatgaagaag	aatttaactg	gaaactactt
3011	actaaaacag	acagagaaaa	aaataggtat	tttaaattta	acgtttaaact	ttatttaagg	gctgatagt
3081	caacacaagc	agaagtgtac	tttaaacgag	ttcgtagtgg	ttactacact	ataaatgaca	ttagagagtg
3151	ggaagattta	ccaccagttg	aagggtggaga	taagccgcta	ataagcgggt	atttatacc	aattgacacg
3221	ccacttgaat	taagaaaatc	tttgaagggt	gggtgataaaa	atgtcaatga	aagctaagta	ttttcaattg
3291	aaaagaaaaa	caaaaagtaa	aggtgaaata	tttatttatg	gtgatattgt	aagtgataaa	tggtttgaaa
3361	gtgatgtaac	tgctacagat	ttcaaaaata	aactagatga	actaggagac	atcagtgaat	tagatgttca
3431	tataaattca	tctggaggca	gtgtatttga	agggcatgca	atatacaata	tgctaaaaat	gcattcctga
3501	aaaatttaata	tctatgtcga	tgcttagcgg	gcattcaattg	ctagtgttat	cgctatgagt	ggtgacacta
3571	tttttatgca	caaaaatagt	tttttaatat	ttcataattc	atgggttatg	actgtaggta	atgcagaaga
3641	gttaagaaag	acagcggatt	tacttgaaaa	aacagatgct	gttagtaatt	cagcttattt	agataaagca
3711	aaagatttag	atcaagaaca	cttaaaacag	atgttagatg	cagaaacttg	gcttactgca	gaagaagcct
3781	tgctcttctg	cttgatagat	gaaattttag	gagctaattga	aataactgct	agtatctcta	aagagcaata
3851	taagcgtttc	gagaaacgtc	cagaagattt	aaagaaagat	gtagacaaaa	tcactaaaaa	cgatgatgta
3921	gatacgtttg	aattgggtga	aacacctaata	gaaagtatgt	cactagaaga	aaaagaaaaa	agagaaaaaa
3991	ttaaacgcga	atgcgaaatt	ttaaaaatga	caatgagtta	ttaggaggaa	atgaaatgcc	gacattatat
4061	gaattaaaaa	aatccttagg	tatgatttga	caacaattaa	aaaaataaaa	tgatgaattg	agtcagaaag
4131	caacagaccc	aaatattgat	atggaagaca	tcaaaaactc	agaaacagaa	aaagcaggct	tacaacaag
4201	atttaacatt	gttgaaagac	aagtaaaaga	cattgaagaa	aaagaaaaag	cgaaagttaa	agacacagga
4271	gaagcttatc	aatcttttaa	tgatcatgag	aagatggtta	aagctaaggc	agagttttat	cgtcacgcga
4341	ttttacaaa	tgaatttgaa	aaaccttcaa	tggaggcaca	acgtttatta	cacgctttac	caacaggtta
4411	tgattcaggt	gggtataagc	tcttaccaaa	aacactttct	aaagaaattg	tttcagaacc	atttgctaaa
4481	aaccaattac	gtgaaaaagc	tcgtctaact	aacattaaag	gttttagagat	tccaagagtt	tcataacttt
4551	tagacgatga	tgacttcatt	acagatgtag	aaacagcaaa	agaattaaaa	ttaaaagggtg	atacaggtta
4621	ttactactact	aataaattca	aagtatttgc	tgcaatttca	gatactgtaa	ttcatggatc	agatgtagat
4691	ttagtataact	gggttgaaaa	cgcactacaa	tcagggtctag	cagctaaaga	acgtaaagat	gccttagcag



4761 taagtccctaa atctggatta gatcacatgt catttttaca tggatctgtt aaagaagttg agggagcaga  
 4831 catgtatgat gctattatta acgcttttagc agattttacat gaagattacc gtgataacgc aacaatttat  
 4901 atgcgatatg cggattatgt caaaattatt agtgttcttt caaatggaac aacaaatttc tttgacacac  
 4971 cagcagaaaa agtattttggc aaaccagtag tattttacaga tgcagcagtt aaacctattg tgggagattt  
 5041 caattattttt ggaattaact atgatggaac aactttatgac actgataaag atgttaaaaa aggcgaatat  
 5111 ttgtttgtat taactgcatg gtatgcatag caacgtacat tagacagtgc attcagaatt gcaaaagcaa  
 5181 aagaaaaatag aggttcatta cccagctaac tctagaagca agttaaag agctaaggct aatatcagctg  
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 5321 atttcgaaaa tgattttaatt gaaggtctca tccaatcggtc taagtctgaa ttactattaa gtgggtttcc  
 5391 agattatgac aaagatgact tgggaatcccc gcttttttgt acagcgatta gatataatcat tgcaagagat  
 5461 tatgaaagac gtgggtactc aaatgaccaa tctagaagca aggtttttta tgaaaaggga ttgcaaaaaa  
 5531 tgattctgaa attaaaaaag tggtaggtga tttttaaatg gaatttaatt aatttaaaga tcgcgcataat  
 5601 ttttttcaat atgtaaaaaa agggccgtat ccagatgaag agggaaaaat gaagttgtat agttgctttt  
 5671 gtaaaatata taatccttct atgaaagata gagaaatttt aaaagcgact gaatcaaagt caggactaac  
 5741 ctaaaatatt aggtcttcta aaattgaata tctaccacaa acaaatcact tagttaaatt ttgcaaaaaa  
 5811 ttatattccg ataaattatt caacattaaa gaaataagaa ttgatacacc agatattggc tataatacag  
 5881 tgggtttatc agaaaaatga gtgtagaagt taaagggata cctgaagtgt tgaagaaatt agaactcggt  
 5951 tacggtaaac aatcaatgca agctaagagt gatagagctt taaatgaagc atctgaattt tttataaagg  
 6021 ctttaaagaa agaattcgag agttttaaag atacgggtgc tagcatagaa gaaattgacta attcctaagg  
 6091 ttatacaaaa gttaggaagtc aagaaagagc tgttttaatt gaatgggtag gccctatgaa tcgcaaaaac  
 6161 attattcact tgaatgaaca tggttataca agagatggaa aaaaatatac accaagaggt tttggagtta  
 6231 ttgcaaaaac attagctgct aatgaacgga agtatagaga aattataaaa aaggagttgg ccagataaat  
 6301 gaatatatta aacaccataa aagaaatttt attactctgat gcagagctcc aaacatatat aaattctaag  
 6371 atatactatt ataaagtcac tgaaaatgct gaaacttcca aaccttttgt tgttattaca cctatttatg  
 6441 atttaccttc agacttcatg tctgataaat atcttagtga agaatactta attcaaatag atgtagaatc  
 6511 ttcaataaat cagaaaacaa ttgatataac aaaacgaata agatatctgt tatatcaaca aaatttaatt  
 6581 caagcatcta gtcagttaga tgcctatttt gaagaacta aacgttatgt gatgtcgaga cgttatcaag  
 6651 gcataccaaa aatatatata tataaaaact agcgcctcga ataggtgtgc tttttaattt taaggaggga  
 6721 aataagcaat ggcagaagga caaggttctt ataaagtagg ttttaaaaga ttatacgttg gagtttttaa  
 6791 cccagaagca acaaaagtag ttaaacgcac gatcatgggaa gatgaaaaag gtggtacagt tgatctaaat  
 6861 atcacaggtt tagcaccaga tttagtagat atgtttgcat ctaacaaacg tgtttggatg aaaaaacaag  
 6931 gtactaatga agttaagtc gacatgagta tttttaatat tccaagtga gatctaaata cgtttattgg  
 7001 tcgttctaaa gataaaaaatg gtacatcttg ggtaggagag aatacaagag caccatacgt aacagttatt  
 7071 ggagaatctg aagatgggtt aacaggtcaa ccagtgtagc ttgctgact taaagggtact tttagcttgg  
 7141 attcaattga atttaaaaac cgaggagaaa aagcagaagc accagagcca acaaaattaa cgtgtgactg  
 7211 gatgaacaga aaagttagtg ttgatgttac tccacaaggt attgtatagc ggtatcatga aggttaagaa  
 7281 ggagaagcag aattcttcaa aaaagtattc gttggataga cggacagtga agatcattca gaggattctg  
 7351 caagttcggt acccagctaa cccccaaat gttgaagtag cagttaattc aaaatctgca acagtttcag  
 7421 cagaataggg gctttcaaaa taaatcaaa gagataaatt tatgactaaa actttaagg tttataaagg  
 7491 agacgagctc gtagcttctg acaaaagtg aggcacaaagtc tcaagtaact tatctaaatt agaaaggatg  
 7561 acaacttctc caaaaggtac ttaccaagtg gctatgggaa aaaatggtaa agaactagat aaagttagt  
 7631 tacctcaatt caaaaccaat ccaattctag tctcaggcgt atcatttaca cccgaaacta aatcaatcac  
 7701 ggtaaatgct gatgacaatg ttgaaccaa cattgcacca agtacagcaa cgaataaaaac gttgaaatat  
 7771 acaagtgaac atccagtagc ttactgtgt gatgagagaa caggagcaat tcacggtgta cgtgagggaa  
 7841 cttcagttat cactgctagc tctactagc gaagtgaaca gtctggacaa attacagtaa gctgaacaaa  
 7911 tggataatta tttgagacgc agaataatct cgtctttttt atttgaataa aaggagctaa tacaatgatt  
 7981 aaatttgaaa tttaagaccg taaaacagga aaaacagaga gctatacaaa agaagatgtg acaatgggag  
 8051 aagcagaaaa atgctatgag tatttagaatt tagtaaatca agagaataaa aaagaagtac ctaacgcaac  
 8121 aaaaatgaga caaaaagagc gacagttatt acaaaagcct tgaagatat atttcgagaa atcaatggtg  
 8191 gttttgaaca agatgagcac taaaacttat acaaaagcct tgaagatat atttcgagaa atcaatggtg  
 8261 aagatgaaga agattcagaa actgaaccag aagagatggg aaagacagaa gaacaaatctc aataaaagat  
 8331 attttatcga acattaaaga aatacaacgt tctctgtatg agcagtatgg gtggacatta actgaagtca  
 8401 gaaaacagcc gtagtgaaaa cttttagaaa ttactaatga agagaataaa gaagagactg aagaaagcaa  
 8471 aagtgaacaa aaagtcatta caggtacgga tttaagaaaa ctttttggaa gctagaaagg aggttaatat  
 8541 gaatgaaaaa gtagaaggca tgaccttggg gctgaaatta gaccttttag gtgtccaaga aggcagtaag  
 8611 gggttaaagc gacaattagg tgtgtttaat agtgaaatga aagctaactc gtcacattt gataagctg  
 8681 aaaaatcaat ggaaaagtat caggcgagaa ttaagggtt aaatgataag cttaaagttc aaaaaagat  
 8751 gtattctcaa gtagaagatg agcttaacaa agttaacgct aattatcaaa aagctaaatc tagtgtaaaa  
 8821 gatgttgaga aagcatattt aaagctagta gaagctaata aaaaagaaaa attagctctt gataaatcta  
 8891 aagaagcctt aaaatcttcg aatacagaac ttaaaaaagc tgaaaatcaa tataaacgta caaatcaacg  
 8961 taacaagatt gcatatcaaa aacttaacaa gttgagagat gcagaaacaa agcttaagaa tagtaacca  
 9031 gctactactg cacaactaaa aagagcaagt gacgcagtag agaagcagtc cgctaagcat aaagcacttg  
 9101 ttgaacaata taaacaagaa ggcaatcaag tcaaaaact aaaagtacaa aatgataatc tttcaaaatc  
 9171 aaacgaaaaa atagaaaatt cttacgctaa aactaatact aaattaaagc aaacagaaaa agaattta  
 9241 gaatttaata atactattaa gaatcatagc caaaagctga aacagctgtg aacaaagaaa aacaaagaaa  
 9311 aagctgcttt aaataattta gagcgttcaa tagataaagc ttcatccgaa atgaagactt ttaacaaaga  
 9381 acaaatgata gctcaaagtc atttcggcaa acttgctagt caagcggatg tcatgtcaaa gaaatttagt  
 9451 tctattggag ataaaatgac ttccctagga cgtacgatga cgatgggctg atctacaccg attactttag  
 9521 ggtaagggtc agcattaaaa acaagtgagc aactcgaagg gcaaatgtct cgagtggag cgtgtgaca  
 9591 agcaagcgtg aaagacttaa aaagcatgtc taattcaagg gttgacttag gcgctaaaaa aagtaaaagt  
 9661 gctaacgaag ttgctaaggc tatggaagaa ttggcagctt taggctttaa tgccaaacaa acaatggagg  
 9731 ctatgccggg tggtatcagt gcagcagaag caagcgggtc agaaatggct acaactgcaa ctgtaatggc  
 9801 atcagcaatt aattctttcg gtttaaaagc atctgatgca aaccatgttg ctgatttact cgcagatca  
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SD-63311.4



Table 8

## Bacteriophage 3A ORFs list

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Table 9

Bacteriophage 96, complete genome sequence

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 39831 ggtaatttta aaaatgtaaa gaagtttatt tacgaagggt aagaatatac aaaagtatat cgtggaata  
 39901 tccaagtatg gaaaaagcct tcacttttg taataaaaac cttacctaaa aataaatatc cgttagcat  
 39971 agaagaatca acagcaaaat ggacaataaa tggagttaa cctaataaaa gttatcaggt gacaatagaa  
 40041 aatgtacgta gcggtataat gagggtttcg caaactaatt taggttcaag tgatttagga atatcaggag  
 40111 tcaatagcgg agttgcaagt aaaaatatca actttagtaa tcttcaggg atgttgatg tcaactaaag  
 40181 tgatgtttat tcaggatctc caacattgac cattgaaata ttttaaacga ctaatttttt agtcgtttt  
 40251 tattttggat aaaaggagca aacaaatgga tgcaaaagta ataacaagat acatcgtatt gatcttagca  
 40321 ttagtaaatc aattcttagc gaacaaaggt attagccga ttccagtaga cgatgagact atatcatcaa  
 40391 taatacttac tgttgttgct ttatatacta cgtataaaga caatccaaca tctcaagaag gcaaatgggc  
 40461 aaatcaaaaag ctaaagaaat ataaagctga aacaagatg agaaaagcaa cagggcaagc gccaaataaa  
 40531 gaagtaatga cacctacgaa tatgaacgac acaaatgatt tagggtaggt gttgaccaat gttgataaca  
 40601 aaaaaccaag cagaaaaatg gtttgataat tcattagggg agcagttcaa tctctgattg ttttatggat  
 40671 ttcagtgtta cgattacgca aatatgtttt ttatgatagc aacaggcgaa aggttacaag gtttatcgc  
 40741 ttataatatt ccatttgata ataaagcaag gattgaaaaa tacgggcaaa taattaaaaa catgatagc  
 40811 tttttaccgc aaaagttgga tattgtcgtt ttcccgtcaa agtatgggtg cggagctgga catgttgaaa  
 40881 ttgttgagag cgcaaattta aacactttca catcatatgg gcaaaattgg aatggtaag gttggacaaa  
 40951 tggcgttgcg caacctggtt ggggtcctga aactgttaca agacatgttc attattacga tgaccaatg  
 41021 tattttatta gattaaattt ccagataaa gagatgtttg gagataaagc taaaagcgtt attaaagcag  
 41091 caactgccaa aaagcaagca gtaattaac ctaaaaaaat tatgcttgta gccggtcatg gttataacga  
 41161 tcttgagca gtaggaaacg gaacaaacga acgcgatttt atccgtaaat atataacgcc aaatatcgct  
 41231 aagtaatttaa gacatgcagg tcatgaagtt gcattatag gtggctcaag tcaatcacaa gacatgtatc  
 41301 agataactgc atacgggtgtt aatgtaggaa ataaataaga ttatggatta tattgggtta aatcacaggg  
 41371 gatgacatt gttctagaga ttcatttaga ccagcagga gaaaatgcaa gtgggtgggca tgttattatc  
 41441 tcaagtcaat tcaatgcgga tactattgat aaaagtatac aagatgttat taaaaataac ttaggacaaa

**BOOKS** **IN** **THE**



Table 10

## Bacteriophage 96 ORFs list

SID	LAN	FRA	POS	a.a.	RBS sequence	STA	STO
100733	96ORF001	1	25999..29142	1047	ccttgaatcgaaaggaggttagcct	ttg	taa
100734	96ORF002	1	32008..33906	632	ttttacgactaaaggaggcaacca	atg	taa
100735	96ORF003	1	30109..31995	628	ttatatttttagataaaggagtagcct	atg	taa
100736	96ORF004	1	36760..38634	624	attttgattgaaatgaggtgcatac	atg	taa
100737	96ORF005	3	33903..35729	608	gtttattcgaaggaaagggtggttga	ata	taa
100738	96ORF006	2	40589..42043	484	aatgatttagggtaggtgttgacca	atg	tag
100739	96ORF007	1	18652..20091	479	tatacacacataactaaacctgaacg	att	tga
100740	96ORF008	2	8960..10201	413	tggcagaatttgggggagataacga	atg	tga
100741	96ORF009	2	17447..18670	407	gacgcaataacggaagtgcgtca	atg	tga
100742	96ORF010	1	38647..39819	390	taaataataataaaggaggtgtgtaa	atg	tga
100743	96ORF011	-1	119..1195	358	gtagctcgccctacccttattatttt	ttg	tga
100744	96ORF012	2	20045..21013	322	tttaatgacaaattacctgacatag	atg	tga
100745	96ORF013	3	29157..30098	313	acttattataaggagggtttggtag	ttg	taa
100746	96ORF014	1	21925..22839	304	agaaaataaagttaggtaataaaat	atg	tag
100747	96ORF015	1	5812..6591	259	atacacggtaaagggtgggagaaatag	atg	taa
100748	96ORF016	1	7852..8607	251	aataaaatgttgaaaggagagaaaa	atg	taa
100749	96ORF017	3	3444..4190	248	aaatttaacattaatatcacttttaa	gtg	taa
100750	96ORF018	-3	28281..29000	239	taagctatgttgaaacatcgctagtc	atg	tga
100751	96ORF019	3	7188..7859	223	ttaccgttctaggacgtggttttaa	atg	taa
100752	96ORF020	3	21324..21908	194	gaaggggcaaaaaggaggtttgatat	atg	taa
100753	96ORF021	3	6612..7175	187	attaaaaataaattaaaaggacggt	ata	tag
100754	96ORF022	2	24536..25093	185	aaagaaaaacgaaggagtgtattaa	atg	taa
100755	96ORF023	1	5275..5811	178	catgaaatggttaggaggtatgaaaa	gtg	tag
100756	96ORF024	3	14481..15014	177	taaaacgtaggagataacgaataa	atg	taa
100757	96ORF025	2	25157..25666	169	ataaaaaaattgaaaagggtatat	att	taa
100758	96ORF026	-3	15084..15590	168	tcattcttaacatagcccttaattc	atg	tga
100759	96ORF027	-1	1229..1732	167	aatagcaataaaaggagtgtaaaac	atg	taa
100760	96ORF028	1	16960..17454	164	aaggcgtgtgatacagtgaaaacaa	ttg	taa
100761	96ORF029	-1	1736..2227	163	tatgagaaaaggagtcataaaaag	atg	taa
100762	96ORF030	1	25531..25995	154	tttcaagagggagagtcgctcgtat	ctg	tag
100763	96ORF031	2	23633..24097	154	tttagtattgaagggtgattctgtag	atc	tag
100764	96ORF032	-2	2248..2706	152	ataagacaccaaagggtttggcgc	atg	tga
100765	96ORF033	-3	39147..39605	152	agcatataaatcgtttagtgtttgt	ttg	taa
100766	96ORF034	2	13181..13615	144	tagaagtcgaaaaagtggaggcaat	ata	taa
100767	96ORF035	2	10628..11053	141	gagctaggattgcaagcaacgatat	ttg	tga
100768	96ORF036	2	24110..24535	141	gtatttttcatagagggtggttaaat	atg	taa
100769	96ORF037	1	12583..12996	137	atgaggaacagaagcaaccaacttt	att	tga
100770	96ORF038	1	15628..16032	134	atgttaagaatgatgcctagttttaa	ttg	taa
100771	96ORF039	3	39816..40220	134	ctaatacactttacttaattaaagg	gtg	taa
100772	96ORF040	-3	27528..27932	134	tttccataaataaacgaggacacca	atg	tga
100773	96ORF041	3	16206..16607	133	gatgagggcgagggtgtcagagtag	atg	tga
100774	96ORF042	2	35720..36106	128	aagttactataactaaaattatggg	gtg	taa
100775	96ORF043	-2	35713..36081	122	ttaaacgtccccctcagttattgtt	ttg	taa
100776	96ORF044	-2	9460..9828	122	agtatccatcagttgaagataatct	ata	taa
100777	96ORF045	-3	5139..5504	121	ttctttttgtattctgtaatttca	att	tga
100778	96ORF046	2	11513..11872	119	aagtaaatgtatagagggtggaataa	atg	taa
100779	96ORF047	2	22991..23350	119	gtcgtactacgtctgataagagcga	gtg	tag
100780	96ORF048	3	8607..8963	118	tggaaaaagaattgagtgatgacta	atg	tga
100781	96ORF049	1	23353..23697	114	atccgtttaaaccaataaaggtagag	gtg	taa
100782	96ORF050	-2	2728..3072	114	tggtaaattagttacattaagta	ata	taa
100783	96ORF051	3	4692..5021	109	tcaaaatatacggaggtagtcaact	atg	tga
100784	96ORF052	-1	20882..21211	109	gtagcaaaagagacaactaaaaaagt	gtg	taa
100785	96ORF053	1	40252..40578	108	acgactaattttttagtcgtttttt	att	tag
100786	96ORF054	1	4942..5262	106	aataaaaaactaaaaaacaaaattt	atg	tag
100787	96ORF055	-2	4840..5151	103	ccgtcgcaatataatagttcgcttaa	atc	taa
100788	96ORF056	3	36324..36623	99	aatttaacacaaaagtaggtggcgta	atg	taa
100789	96ORF057	2	1394..1690	98	cttcagtggtctcttttagcatttaa	ata	taa
100790	96ORF058	-3	26247..26537	96	tacttcttttctcataatctgacca	att	tga
100791	96ORF059	-1	21485..21772	95	agactcaacgcctttttgaacatac	ttg	tga
100792	96ORF060	-3	22647..22931	94	cctctttgttaaccgacaagactgta	ata	taa
100793	96ORF061	1	14023..14304	93	ttatctaattaagggggacgagtgta	gtg	taa



100794	96ORF062	-2	38281..38559	92	tatataacttagcgattgtacttgc	ttg	taa
100795	96ORF063	-3	30786..31064	92	gtctcctaatactacatcttgctta	gtg	tga
100796	96ORF064	-2	30205..30480	91	atgcatctacttttggtgtaatac	ata	tag
100797	96ORF065	1	2617..2886	89	aagggtctaataaaaatttctccttc	ttg	taa
100798	96ORF066	3	28056..28325	89	aagggtgtagtcggctggttaactga	att	taa
100799	96ORF067	-3	17142..17411	89	ttccggtatttgcgtcgtgaagtgt	ttg	tga
100800	96ORF068	2	12326..12589	87	aatgcatgtcgtttggtctgcctaa	ttg	tag
100801	96ORF069	2	42734..42997	87	tttttaggcaacgatataagtaaaa	gtg	taa
100802	96ORF070	1	11869..12129	86	aaatgttcaagaaatggagtgaagc	ata	taa
100803	96ORF071	3	15396..15656	86	aacaagctatacaaaattatcgataa	att	taa
100804	96ORF072	-3	37749..38009	86	agattttttcgggttacccttagac	att	taa
100805	96ORF073	3	11244..11501	85	acatgcataatagagggtggaataa	atg	tag
100806	96ORF074	-3	42936..43193	85	aattatttaacttactaattttctt	ttg	taa
100807	96ORF075	-3	26610..26867	85	tactgccaatgttccatcttcaacc	att	taa
100808	96ORF076	-1	11126..11380	84	tttatctaatacatttaagttaacc	atc	taa
100809	96ORF077	-2	16537..16791	84	taccaccatataaggcaggtagtag	gtg	tag
100810	96ORF078	-3	19521..19775	84	aataactttgaattgatacctcaac	ata	tga
100811	96ORF079	3	13608..13859	83	ttagggaatggaggcagacacaa	atg	tag
100812	96ORF080	-3	28029..28280	83	tgagaagtgcgcagtaagcaactga	att	tga
100813	96ORF081	3	20973..21221	82	aatgaagtatccattcatgactt	atc	tag
100814	96ORF082	-1	8729..8974	81	cgattattgtgctttcaatttcaa	ttg	tga
100815	96ORF083	-3	3147..3392	81	tttagcctttatataatcaacttct	gtg	tga
100816	96ORF084	3	1611..1853	80	tgctttatctttagtttcttctt	ttg	tga
100817	96ORF085	-2	29470..29709	79	ctcttatcaccttcgtttgtaggca	atc	taa
100818	96ORF086	1	35188..35424	78	gcgcaaggcgatttgggatatttaa	ctg	tag
100819	96ORF087	-2	13039..13275	78	ttttgattgagctctaaagtgtctt	att	tag
100820	96ORF088	3	24930..25163	77	gaactatcattaaaagttaaatgga	ata	tga
100821	96ORF089	-3	22329..22562	77	tcagataagatagtggttaatccc	ata	taa
100822	96ORF090	-3	16803..17036	77	acctttagtccaataccctgcgtca	ata	tag
100823	96ORF091	-1	22559..22789	76	aacgcttctggtttaacgttcatgt	atg	taa
100824	96ORF092	3	18360..18587	75	attgcaaaagatattgtaagttagat	atg	taa
100825	96ORF093	-2	25384..25608	74	catgatttcttctgtaattctctt	atc	taa
100826	96ORF094	1	10417..10638	73	aacacacattaaggagtgttaaaaa	atg	tag
100827	96ORF095	3	12963..13184	73	tactaaacgaagataaaaactatgac	att	taa
100828	96ORF096	1	42994..43212	72	gatcgcttgaaaacgaagaagataa	ata	taa
100829	96ORF097	-1	36047..36265	72	tcaagcattacacctgtgacttttc	atc	taa
100830	96ORF098	-2	36766..36984	72	cagggtccggtacaaatccagatga	ata	taa
100831	96ORF099	-2	34765..34983	72	tcattctttttataaaaacgggtacc	atg	tag
100832	96ORF100	1	10198..10413	71	acaagaagactcagaggtttttcac	atg	taa
100833	96ORF101	1	15208..15423	71	gagaaacaagttaagataaggagag	atg	tga
100834	96ORF102	3	4209..4424	71	attttaaaacgaatataggagagg	ctg	tag
100835	96ORF103	3	11673..11888	71	catgcaccttatgggtatgcgcttag	ctg	taa
100836	96ORF104	3	12117..12332	71	tttagctccaaagagcttttgactt	gtg	taa
100837	96ORF105	3	23892..24107	71	gatgggtgggttatccagtgtataa	gtg	taa
100838	96ORF106	-3	34428..34643	71	tagacttttgccaatttgttgttga	att	taa
100839	96ORF107	-3	24495..24710	71	ggcacattaccaattgttaatttaa	atg	taa
100840	96ORF108	-1	23876..24088	70	acatatttaaccacctctatgaaaa	ata	taa
100841	96ORF109	-2	17317..17529	70	acctgtacgcttgcctcggtgatta	att	taa
100842	96ORF110	-3	38931..39143	70	actttcattcttttcgatgtaagaa	atg	taa
100843	96ORF111	-3	21855..22067	70	agtaaatttttcttttgcgtgtc	att	tga
100844	96ORF112	1	3217..3426	69	aaatgtcaacgggaggtgatacgaa	atg	taa
100845	96ORF113	-1	25469..25678	69	tcagggatataatcctaataatctag	ctg	taa
100846	96ORF114	-2	9838..10047	69	ataataatcatcacggtaaagtacg	atc	tga
100847	96ORF115	1	13819..14022	67	gcagtaggggttatggcagggtcaag	ttg	tga
100848	96ORF116	-1	41033..41236	67	caacttcatgacctgcatgtcttaa	ata	taa
100849	96ORF117	-3	24711..24914	67	tctgctgtattccatttaactttta	atg	taa
100850	96ORF118	-1	12374..12574	66	tccatctcctctaaaaataaagtgg	ttg	taa
100851	96ORF119	-1	3980..4180	66	ctctatatcttgcgtttttaaatttc	att	tga
100852	96ORF120	-3	6033..6233	66	ttgtaatttagaaatataacgataa	ata	taa
100853	96ORF121	-2	37939..38136	65	ctgaaatgccttgatactgcctaa	att	tga
100854	96ORF122	2	37892..38086	64	acgacaaaaacaacaataagaatta	gtg	tga
100855	96ORF123	-3	29193..29387	64	ggacgtctgactttaaatgtgaagc	ata	tga
100856	96ORF124	1	4408..4599	63	ttatcggtaccatttaagtatta	atg	taa
100857	96ORF125	-1	7787..7978	63	ttaaaaatccaagttttgccatcgt	att	tga
100858	96ORF126	-3	27027..27218	63	aaatttgaacaacggcatttaattga	gtg	tga
100859	96ORF127	3	15051..15239	62	atcgagtcaaggaggttttggggaa	gtg	tga
100860	96ORF128	-1	6914..7102	62	agcgaatgggtttgattgtgactc	ata	tga
100861	96ORF129	-3	31332..31520	62	tcttatttgcctctgcttctataa	atg	tga
100862	96ORF130	-3	30084..30272	62	gaaatcatcttccacttcaacatga	gtg	taa
100863	96ORF131	3	11058..11243	61	agaaaaagagaaatgaagtgatcta	atg	taa
100864	96ORF132	-1	36434..36619	61	taagcatggtaatcacctcctttaa	ata	tga

100865	96ORF133	-1	35591..35776	61	ctaaactattgcgtaaacccgccagt	att	taa
100866	96ORF134	-2	9250..9435	61	atccatgagcttataaaccgctcta	att	tga
100867	96ORF135	1	29563..29745	60	cgacaactttttgtaggactagtaa	gtg	tga
100868	96ORF136	-3	12486..12668	60	cactttactttcaactgttcagga	ttg	taa
100869	96ORF137	-1	14501..14680	59	caaactgaaagctaagtaatacagca	atc	tga
100870	96ORF138	-2	23326..23505	59	cttgtagacatttgatgaatttttag	ttg	tga
100871	96ORF139	-3	42672..42851	59	aatccggaatttttagcaattttat	atc	taa
100872	96ORF140	-3	31137..31316	59	acttgattgactagtaaagtcgtac	atg	taa
100873	96ORF141	-3	18969..19148	59	aacaaaaataacattatagggatct	ata	taa
100874	96ORF142	-3	4740..4919	59	cataaattttgttttttagttttat	att	tga
100875	96ORF143	2	36107..36283	58	aacaaataactgaggggacgtttaa	atg	taa
100876	96ORF144	3	16029..16205	58	tatacgaagtaaagaaggtagataa	ata	tag
100877	96ORF145	-3	29013..29189	58	tgctactgacgcgatactgtgaacc	att	tga
100878	96ORF146	-3	14883..15059	58	aatccttgatgttgtagtaagta	ttg	taa
100879	96ORF147	-1	18251..18424	57	tatcagcgtaattgcacgtaact	atg	taa
100880	96ORF148	-1	13583..13756	57	aataccttctttaactgaatgttga	ata	taa
100881	96ORF149	-2	10756..10929	57	taaatcacatctctatactgat	ctg	tag
100882	96ORF150	2	14171..14341	56	attttaataagaagtggttattaa	ctg	tag
100883	96ORF151	2	19217..19387	56	cctacatactcattgcgctactttt	atg	tga
100884	96ORF152	-1	12614..12784	56	atttctacagtaaaaaatctttat	ctg	taa
100885	96ORF153	-2	11836..12006	56	ttgcattacctattgcgaatgctag	ttg	taa
100886	96ORF154	-2	4165..4335	56	atataacgcttttgcctcgaccaa	atc	tga
100887	96ORF155	-3	40464..40634	56	aaatcaggattgaactgcttccta	atg	tga
100888	96ORF156	3	423..590	55	tggttaattttgataatttagcttta	ata	taa
100889	96ORF157	-1	41879..42046	55	gtagcaaaatttttattctaagtaa	ata	taa
100890	96ORF158	-2	36166..36333	55	cattcatgttcgtgccgtttggtaa	atc	tag
100891	96ORF159	-2	16228..16395	55	tttaacatctgagcatacctttat	ttg	taa
100892	96ORF160	3	1038..1202	54	atctctaagcagttgttgagcagcg	ttg	taa
100893	96ORF161	-1	19193..19357	54	tctttgtgttaggtacaccaaca	atg	tag
100894	96ORF162	-1	18074..18238	54	ctcgtcctattaacacaatagatcc	ata	tga
100895	96ORF163	-1	15386..15550	54	agccatcataggactgtaaaattca	ctg	taa
100896	96ORF164	-1	10049..10213	54	tacatcgatttcaataagcttttga	att	tag
100897	96ORF165	-2	18514..18678	54	gtgcttcaatatcatctattaaact	ata	taa
100898	96ORF166	-2	11104..11268	54	ctagccatgattacccttaaattag	ttg	tag
100899	96ORF167	-3	13764..13928	54	agacagtttataatgtgtatctcta	ata	tga
100900	96ORF168	1	14305..14466	53	ttttgaatttttgaggacgagtaa	atg	tag
100901	96ORF169	-1	17885..18046	53	gtgttgaagccttaatagactcttt	ata	tga
100902	96ORF170	-1	10790..10951	53	taggcgctttacatatccacgttaa	att	taa
100903	96ORF171	-3	12765..12926	53	atcttcgttttagtatataaaacgct	ctg	taa
100904	96ORF172	3	22836..22994	52	cgttcgcaacgcttaaaccaactga	ata	tga
100905	96ORF173	-1	15956..16114	52	ctctacatcatcattagccgtcgtc	ata	taa
100906	96ORF174	-1	10571..10729	52	tagtgccattcatattactttctaa	ata	taa
100907	96ORF175	-1	3440..3598	52	cagcctatcttcactatcaacatga	ttg	taa
100908	96ORF176	-3	37170..37328	52	tttatctaaaacattgctgtaagca	gtg	taa
100909	96ORF177	-3	6693..6851	52	ttcctaactactaagtaactcgat	ata	taa
100910	96ORF178	-3	5655..5813	52	gacatcttgattagttttttcagtc	atc	tag
100911	96ORF179	1	34564..34719	51	gttacagctgaagtcgataaaatag	ttg	tag
100912	96ORF180	1	42661..42816	51	atataaattctaacactaaactact	atg	tga
100913	96ORF181	-2	37741..37896	51	tggacgcactgtcaactgatgtttt	atc	taa
100914	96ORF182	-2	25039..25194	51	ttcgtaatctttttctccgctatta	att	tga
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101124	96ORF392	2	39287..39388	33	aaaaacggtactgtagtatcaatca	atc	tag
101125	96ORF393	3	18153..18254	33	gtagtatatgccgactttgatttga	atg	taa
101126	96ORF394	3	24189..24290	33	tcagaccctaacattaacaaactag	ttg	tga
101127	96ORF395	-1	15266..15367	33	tcgataatttgtatagcttgtttta	atg	tag
101128	96ORF396	-2	32239..32340	33	ttttagtgaagcatctagtgttga	ata	tag
101129	96ORF397	-2	16123..16224	33	ttatgtgtgcctatcatattaacaa	ttg	tag
101130	96ORF398	-2	13648..13749	33	tctttaactgaatgttgaatagcat	ttg	tag
101131	96ORF399	-2	10987..11088	33	acttctgtaggatttcttatatcaa	ttg	tga
101132	96ORF400	-2	3382..3483	33	cttactggtaattcttcaaaattaa	atg	taa
101133	96ORF401	-3	40794..40895	33	ccatatgatgtgaaagtgtttaa	ttg	taa
101134	96ORF402	-3	39978..40079	33	atattcctaatacactgaacctaa	att	tga
101135	96ORF403	-3	38607..38708	33	atcttcagtgtaaaatcgacagcca	atg	tag
101136	96ORF404	-3	21288..21389	33	cagacaccgtcttaagtcctttag	ata	taa

Table 11

## SEQUENCE INFORMATION FOR PHAGES MATCHING WITH TABLE 1

M32695

Bacteriophage PM2 nuclease cleavage site

gi|166145|gb|M32695|BM2NCS [166145]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

M32693

Bacteriophage PM2 Hind III fragment 4

gi|166144|gb|M32693|BM24HIND3 [166144]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

M32693

Bacteriophage PM2 Hind III fragment 4

gi|166144|gb|M32693|BM24HIND3 [166144]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

M32694

Bacteriophage PM2 Hind III fragment 3

gi|166143|gb|M32694|BM23HIND3 [166143]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

M26134

Bacteriophage PM2 structural protein gene containing purine/pyrimidine rich regions and anti-Z-DNA-IgG binding regions, complete cds

gi|289360|gb|M26134|BM2PROTIV [289360]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

J02452

bacteriophage fi 3'-terminal region ma

gi|215409|gb|J02452|PFITR3 [215409]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

AF020798

Bacteriophage Chp1 genome DNA, complete sequence

gi|217761|dbj|D00624|BCP1 [217761]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 12 protein links, or 1 genome link )

X72793

Clostridium botulinum C phage BONT/C1, ANTP-139, ANTP-33, ANTP-17, ANTP-70 genes and ORF-22

gi|516171|emb|X72793|CBCBONT [516171]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 6 protein links, or 4 nucleotide neighbors )

X51464

Clostridium botulinum D Phage C3 gene for exoenzyme C3

gi|14907|emb|X51464|CBDPE3 [14907]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors )

D90210

Bacteriophage c-st (from C. botulinum) C1-tox gene for botulinum C1 neurotoxin

gi|217780|dbj|D90210|CSTC1TOX [217780]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

S49407

type D neurotoxin [bacteriophage d-16 phi, host = C. botulinum, type D, CB16, Genomic, 4087 nt]  
gi|260238|gb|S49407|S49407 [260238]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

X53370

Bacteriophage phi29 temperature sensitive mutant TS2(98) DNA polymerase gene

gi|15733|emb|X53370|POTS298 [15733]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 7 nucleotide neighbors )

X53371

Bacteriophage phi29 temperature sensitive mutant TS2(24) DNA polymerase gene

gi|15731|emb|X53371|POTS224 [15731]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 7 nucleotide neighbors )

X05973

Bacteriophage phi29 prohead RNA

gi|15680|emb|X05973|POP29PRO [15680]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 4 nucleotide neighbors )

V01155

Left end of bacteriophage phi-29 coding for 15 potential proteins Among  
these are the terminal protein and the proteins encoded by the genes 1, 2 (sus), 3, and (probably) 4

gi|15659|emb|V01155|POP29B [15659]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 16 protein links, or 16 nucleotide neighbors)

X73097

Bacteriophage phi-29 left origin of replication

gi|312194|emb|X73097|BP29ORIL [312194]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors )

M14430

Bacteriophage phi-29 gene-17 gene, complete cds

gi|215321|gb|M14430|P29G17A [215321]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 6 protein links, or 8 nucleotide neighbors )

M14431

Bacteriophage phi-29 gene-16 gene, complete cds

gi|215319|gb|M14431|P29G16A [215319]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 7 nucleotide neighbors )

M20693

Bacteriophage phi-29 DNA, 3' end

gi|215343|gb|M20693|P29REPINB [215343]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 nucleotide neighbors )

M21016

Bacteriophage phi-29 DNA, 5' end

gi|215342|gb|M21016|P29REPINA [215342]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

## M12456

Bacteriophage phi-29 genes 9, 10 and 11 encoding p9 tail, incomplete, p10 connector, complete, and p11 lower collar, incomplete, respectively  
gi|215338|gb|M12456|P29P9 [215338]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 2 nucleotide neighbors )

## M14782

Bacillus phage phi-29 head morphogenesis, major head protein, head fiber protein, tail protein, upper collar protein, lower collar protein, pre-neck appendage protein, morphogenesis(13), lysis, morphogenesis(15), encapsidation genes, complete cds  
gi|215323|gb|M14782|P29LATE2 [215323]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 11 protein links, or 11 nucleotide neighbors)

## M26968

Bacteriophage phi-29 (from Bacillus subtilis) proteins p1 delta-1 genes, complete cds, and the sus1(629) mutation  
gi|341558|gb|M26968|P29P1D1A [341558]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

## J02448

Bacteriophage f1, complete genome  
gi|166201|gb|J02448|F1CCG [166201]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, 205 nucleotide neighbors, or 1 genome link )

## M24832

Bacteriophage f2 coat protein gene, partial cds  
gi|166228|gb|M24832|F2CRNACA [166228]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

## J02451

Bacteriophage fd, strain 478, complete genome  
gi|215394|gb|J02451|PFDCG [215394]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 MEDLINE links, 10 protein links, 204 nucleotide neighbors, or 1 genome link )

## M34834

Bacteriophage fr replicase gene, 5' end  
gi|166139|gb|M34834|BFRREGRA [166139]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 9 nucleotide neighbors )

## M38325

Bacteriophage fr replicase gene, 5' end  
gi|166137|gb|M38325|BFRREGRA [166137]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 9 nucleotide neighbors )

## M35063

Bacteriophage fr coat protein replicase cistron (R region) RNA  
gi|166134|gb|M35063|BFRRCRRA [166134]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 3 nucleotide neighbors )

## S66567

alpha-atrial natriuretic factor/coat protein=fusion polypeptide [human, bacteriophage fr, expression vector pFAN15, PlasmidSyntheticRecombinant, 510 nt]  
gi|435742|gb|S66567|S66567 [435742]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 15 nucleotide neighbors )



## X15031

Bacteriophage fr RNA genome

gi|15071|emb|X15031|LEBFRX [15071]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, 9 nucleotide neighbors, or 1 genome link )

## U51233

Mus musculus neutralizing anti-RNA-bacteriophage fr immunoglobulin variable region light chain (IgM) mRNA, partial cds

gi|1277150|gb|U51233|MMU51233 [1277150]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 1669 nucleotide neighbors )

## U51232

Mus musculus neutralizing anti-RNA-bacteriophage fr immunoglobulin variable region heavy chain (IgM) mRNA, partial cds

gi|1277148|gb|U51232|MMU51232 [1277148]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 1073 nucleotide neighbors )

## U02303

Bacteriophage If1, complete genome

gi|3676280|gb|U02303|B2U02303 [3676280]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,10 protein links, or 1 genome link )

## V00604

Phage M13 genome

gi|14959|emb|V00604|INM13X [14959]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, or 205 nucleotide neighbors )

## A32252

Synthetic bacteriophage M13 protein III probe

gi|1567340|emb|A32252|A32252 [1567340]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## A32251

Synthetic bacteriophage M13 protein III probe

gi|1567339|emb|A32251|A32251 [1567339]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## M12465

Bacteriophage M13 mp10 mutations in lac operon

gi|215210|gb|M12465|M13LACMUT [215210]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 215 nucleotide neighbors )

## M24177

Synthetic Bacteriophage M13 (clone M13.SV.B12) SV40 early promoter region DNA

gi|209416|gb|M24177|SYNSVB12 [209416]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

## M24176

Synthetic Bacteriophage M13 (clone M13.SV.B11) SV40 early promoter region DNA

gi|209415|gb|M24176|SYNSVB11 [209415]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

## M24175

Synthetic Bacteriophage M13 (clone M13.SV.8) SV40 early promoter region DNA

gi|208806|gb|M24175|SYNM13SV8 [208806]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 242 nucleotide neighbors )

## M19979

Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33

gi|207813|gb|M19979|SYN33M13M [207813]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 617 nucleotide neighbors )

## M19565

Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33

gi|207808|gb|M19565|SYN33M13H [207808]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 567 nucleotide neighbors )

## M19564

Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33

gi|207807|gb|M19564|SYN33M13G [207807]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 12 nucleotide neighbors )

## M19563

Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33

gi|207806|gb|M19563|SYN33M13F [207806]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 262 nucleotide neighbors )

## M19561

Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33

gi|207804|gb|M19561|SYN33M13D [207804]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 27 nucleotide neighbors )

## M19560

Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33

gi|207803|gb|M19560|SYN33M13C [207803]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## M19559

Synthetic hybrids; recombinant DNA from bacteriophage M13 and plasmid pHV33

gi|207802|gb|M19559|SYN33M13B [207802]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 227 nucleotide neighbors )

## M10568

Bacteriophage M13 replicative form II, replication origin, specific nick location

gi|215220|gb|M10568|M13ORIB [215220]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 650 nucleotide neighbors )

## M10910

Bacteriophage M13 gene II regulatory region and M13sj1 mutant

gi|215209|gb|M10910|M13IIREG [215209]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 72 nucleotide neighbors )

## M38295

Bacteriophage M13 HaeIII restriction fragment DNA

gi|215208|gb|M38295|M13HAEIII [215208]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 67 nucleotide neighbors )

## E02067

DNA encoding a part of Bacteriophage M13 tg 127

gi|2170311|dbj|E02067|E02067 [2170311]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## J02467

Bacteriophage MS2, complete genome

gi|215232|gb|J02467|MS2CG [215232]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,8 MEDLINE links, 4 protein links, 20 nucleotide neighbors, or 1 genome link )

## AJ004950

Bacteriophage P1 ban gene

gi|3688226|emb|AJ011592|BP1011592 [3688226]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link )

## U88974

Bacteriophage P1 structural lytic transglycosylase (orf47), pep44b (orf44b), pep44a (orf44a), and pep43 (orf43) genes, complete cds; and pep42 (orf42) gene, partial cds

gi|2661099|gb|AF035607|AF035607 [2661099]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 protein links, or 1 nucleotide neighbor )

## AJ000741

Bacteriophage P1 darA operon

gi|2462938|emb|AJ000741|BPAJ7641 [2462938]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, or 31 nucleotide neighbors)

## X01828

Bacteriophage P1 recombinase gene cin

gi|15133|emb|X01828|MYP1CIN [15133]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

## X98146

Bacteriophage P1 DNA sequence around the Op88 operator

gi|1359513|emb|X98146|BP1OP88OP [1359513]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor )

## S61175

immI operon: icd=cell division repressor, ant1=antirepressor {promoters

P51a, P51b} [bacteriophage P1, Genomic, 728 nt]

gi|385908|gb|S61175|S61175 [385908]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors )

## X87824

Bacteriophage P1 gene 26

gi|861164|emb|X87824|XXBP1G26 [861164]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link )

## X15638

Phage P1 DNA for lytic replicon containing promoter P53 and two open reading frames

gi|15735|emb|X15638|PP1LREP [15735]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 24 nucleotide neighbors )

## X17512

Bacteriophage P1 DNA for immunity region immI

gi|15479|emb|X17512|P1IMMUNITY [15479]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 4 nucleotide neighbors )

## X16005

Bacteriophage P1 c1 gene for P1c1 repressor protein

gi|15477|emb|X16005|P1C1 [15477]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

## X03453

Bacteriophage P1 cre gene for recombinase protein

gi|15135|emb|X03453|MYP1CRE [15135]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 12 nucleotide neighbors )

## X06561

Bacteriophage P1 c1 gene 5'-region

gi|15128|emb|X06561|MYP1C1 [15128]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 6 nucleotide neighbors )

## V01534

Bacteriophage P1 genome fragment (IS2 insertion spot). This regions contains four unidentified reading frames and is known as insertion hot spot for IS2 insertion sequences

gi|15118|emb|V01534|MYOVP1 [15118]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 3 nucleotide neighbors )

## X56951

Bacteriophage P1 gene10

gi|406728|emb|X56951|BPP1GP10 [406728]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 3 protein links, or 1 nucleotide neighbor )

## K02380

Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC incompatibility determinants

gi|215652|gb|K02380|PP1REP [215652]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 MEDLINE links, 4 protein links, or 8 nucleotide neighbors )

## X87674

Bacteriophage P1 lydA & lydB genes

gi|974763|emb|X87674|BACP1LYD [974763]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link; 2 protein links, or 2 nucleotide neighbors )

## X87673

Bacteriophage P1 gene 17

gi|974761|emb|X87673|BACP117 [974761]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## M16618

Bacteriophage P1 c1 repressor binding sites

gi|215600|gb|M16618|PP1C1 [215600]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors )

## SEG\_PP1CIN

Bacteriophage P1 cin gene encoding recombinase, cixL recombination site, and 5' end of C invertible element

gi|215607|gb|SEG\_PP1CIN [215607]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

## K03173

Bacteriophage P1 C invertible element, right end, and cixR recombination site

gi|215606|gb|K03173|PP1CIN2 [215606]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## 215605

Bacteriophage P1 cin gene encoding recombinase, cixL recombination site, and 5' end of C invertible element

gi|215605|lcl|X01828 [215605]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## M25470

Bacteriophage P1 tail fiber protein gene, complete cds

gi|341349|gb|M25470|PP1TFPR [341349]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 3 nucleotide neighbors )

## M34382

Bacteriophage P1 sim region proteins, complete cds

gi|215661|gb|M34382|PP1SIM [215661]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links )

## M81956

Bacteriophage P1 R protein (R) gene, complete cds

gi|215658|gb|M81956|PP1RP [215658]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 4 nucleotide neighbors )

## M37080

Bacteriophage P1 mini-P1 plasmid origin of replication

gi|215657|gb|M37080|PP1REPOR [215657]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 46 nucleotide neighbors )

## M27041

Bacteriophage P1 ref gene, complete cds

gi|215650|gb|M27041|PP1REF [215650]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## L01408

Bacteriophage P1 partition protein (parB) gene, 3' end

gi|215642|gb|L01408|PP1PARB [215642]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 41 nucleotide neighbors )

## SEG\_PP1PAR

Bacteriophage miniplasmid P1 parA gene, 5' end

gi|215639|gb|SEG\_PP1PAR [215639]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 48 nucleotide neighbors )

## M36425

Bacteriophage miniplasmid P1 parB gene, 3' end

gi|215638|gb|M36425|PP1PAR2 [215638]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M36424

Bacteriophage miniplasmid P1 parA gene, 5' end  
 gi|215637|gb|M36424|PP1PAR1 [215637]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M11129

Bacteriophage P1 miniplasmid origin of replication region  
 gi|215632|gb|M11129|PP1ORIM [215632]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 43 nucleotide neighbors )

M25414

Bacteriophage P1 c1 repressor binding site, operator 88 (Op88)  
 gi|215631|gb|M25414|PP1OP88A [215631]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors )

M25413

Bacteriophage P1 c1 repressor binding site, operator 68 (Op68)  
 gi|215630|gb|M25413|PP1OP68A [215630]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

M25412

Bacteriophage P1 c1 repressor binding site, operator 21 (Op21)  
 gi|215629|gb|M25412|PP1OP21A [215629]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

M10510

Bacteriophage P1 recombination site loxR  
 gi|215628|gb|M10510|PP1LOXR [215628]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

M10287

Bacteriophage P1 loxP X loxP recombination site  
 gi|215627|gb|M10287|PP1LOXPX [215627]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors )

M10494

Bacteriophage P1 recombination site loxP  
 gi|215626|gb|M10494|PP1LOXP [215626]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 134 nucleotide neighbors )

M10511

Bacteriophage P1 recombination site loxL  
 gi|215625|gb|M10511|PP1LOXL [215625]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

M10512

Bacteriophage P1 recombination site loxB  
 gi|215624|gb|M10512|PP1LOXB [215624]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

M10145

Bacteriophage P1 genome fragment with recombination site loxP  
 gi|215623|gb|M10145|PP1CREX [215623]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 21 nucleotide neighbors )

## M13327

Bacteriophage P1 Cin recombinase activated cross over site, junction IV, clone pSHI326  
gi|215622|gb|M13327|PP1CN26IV [215622]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M13325

Bacteriophage P1 Cin recombinase activated cross over site, junction II, clone pSHI326  
gi|215621|gb|M13325|PP1CN26II [215621]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1401 nucleotide neighbors )

## M13323

Bacteriophage P1 Cin recombinase activated cross over site, junction IV, clone pSHI325  
gi|215620|gb|M13323|PP1CN25IV [215620]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M13321

Bacteriophage P1 Cin recombinase activated cross over site, junction II, clone pSHI325  
gi|215619|gb|M13321|PP1CN25II [215619]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1058 nucleotide neighbors )

## M13324

Bacteriophage P1 Cin recombinase activated cross over site, junction I, clone pSHI326  
gi|215618|gb|M13324|PP1CIR26I [215618]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M13319

Bacteriophage P1 Cin recombinase activated cross over site, right junction, clone pSHI327  
gi|215617|gb|M13319|PP1CIN27R [215617]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M13320

Bacteriophage P1 Cin recombinase activated cross over site, junction I, clone pSHI325  
gi|215616|gb|M13320|PP1CIN25I [215616]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M13318

Bacteriophage P1 Cin recombinase activated cross over site, left junction, clone pSHI324  
gi|215615|gb|M13318|PP1CIN24L [215615]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1370 nucleotide neighbors )

## M13317

Bacteriophage P1 Cin recombinase activated cross over site, right junction, clone pSHI323  
gi|215614|gb|M13317|PP1CIN23M [215614]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1055 nucleotide neighbors )

## M13316

Bacteriophage P1 Cin recombinase activated cross over site, left junction, clone pSHI323  
gi|215613|gb|M13316|PP1CIN23L [215613]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M13315

Bacteriophage P1 Cin recombinase activated cross over site, right junction, clone pSHI322  
gi|215612|gb|M13315|PP1CIN22R [215612]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M13314

Bacteriophage P1 Cin recombinase activated cross over site, left junction, clone pSHI322

gi|215611|gb|M13314|PP1CIN22L [215611]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1401 nucleotide neighbors )

## M13313

Bacteriophage P1 Cin recombinase activated cross over site, right junction, clone pSHI321

gi|215610|gb|M13313|PP1CIN21R [215610]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M13312

Bacteriophage P1 Cin recombinase activated cross over site, left junction, clone pSHI321

gi|215609|gb|M13312|PP1CIN21L [215609]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1058 nucleotide neighbors )

## M16568

Bacteriophage P1 c4 repressor gene, complete cds

gi|215603|gb|M16568|PP1C4 [215603]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

## M13326

Bacteriophage P1 Cin recombinase activated cross over site, junction III, clone pSHI326

gi|215602|gb|M13326|PP1C26III [215602]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1192 nucleotide neighbors )

## M13322

Bacteriophage P1 Cin recombinase activated cross over site, junction III, clone pSHI325

gi|215601|gb|M13322|PP1C25III [215601]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1231 nucleotide neighbors )

## J05651

Bacteriophage P1 modulator protein (bof) gene, complete cds

gi|215598|gb|J05651|PP1BOFY1 [215598]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

## M33224

Bacteriophage P1 regulatory protein (bof) gene, complete cds

gi|215596|gb|M33224|PP1BOFFO [215596]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

## M10288

E.coli/bacteriophage P1 loxR recombination site

gi|146647|gb|M10288|ECOLOXR [146647]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors )

## M10289

E.coli/bacteriophage P1 loxL recombination site

gi|146646|gb|M10289|ECOLOXL [146646]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )

## M10290

E.coli loxB site, which can recombine with bacteriophage P1 loxP site

gi|146645|gb|M10290|ECOLOXB [146645]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )



M10287

Bacteriophage P1 loxP X loxP recombination site

gi|215627|gb|M10287|PP1LOXPX [215627]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors )

M74046

Bacteriophage P1 pacA and pacB genes, complete cds

gi|215634|gb|M74046|PP1PACAB [215634]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links )

M95666

Bacteriophage P1 gene 10, doc and phd genes, complete cds

gi|463276|gb|M95666|PP1PHDDOC [463276]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 4 protein links, or 1 nucleotide neighbor )

M25604

Bacteriophage Q-beta mutated autonomously replicating sequence MDV1 RNA fragment

gi|556359|gb|M25604|PQBARSMUT [556359]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 8 nucleotide neighbors )

V00643

first half of the phage Q-beta gene for coat protein

gi|15088|emb|V00643|LEQBET [15088]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

M25167

Bacteriophage Q-beta RNA fragment recovered from replicase binding complex

gi|556362|gb|M25167|PQBREPLICB [556362]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )

M24876

Bacteriophage Q-beta replicase RNA, 5' end

gi|556360|gb|M24876|PQBREPLICA [556360]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

M25444

Synthetic bacteriophage Q-beta DNA

gi|209118|gb|M25444|SYNPQBTERM [209118]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 8 nucleotide neighbors )

M25463

Bacteriophage Q-beta self-replicating microvariant (+) RNA

gi|532489|gb|M25463|PQBMVSRRNA [532489]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

M25014

Bacteriophage Q-beta RNA replicase gene, 5'end, and maturation protein gene, 3' end

gi|294316|gb|M25014|PQBREPLC [294316]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

M25065

Bacteriophage Q-beta RNA sequence with putative stem loop

gi|294315|gb|M25065|PQBLOOP [294315]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors)

M10265

Bacteriophage Q-beta RNA molecule with the ability to replicate extracellularly

gi|215726|gb|M10265|PQBRNA [215726]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 8 nucleotide neighbors )

M24815

Bacteriophage Q-beta specified replicase subunit RNA,

gi|215725|gb|M24815|PQBREPL [215725]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 nucleotide neighbors )

M25461

Bacteriophage Q-beta plus-strand RNA, 5' terminus

gi|215724|gb|M25461|PQBPS5E [215724]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M25462

Bacteriophage Q-beta plus-strand RNA, 3' terminus

gi|215723|gb|M25462|PQBPS3E [215723]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 8 nucleotide neighbors )

M24871

Bacteriophage Q-beta nanovariant WSIII RNA

gi|215722|gb|M24871|PQBNVWSIC [215722]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )

M24870

Bacteriophage Q-beta nanovariant WSII RNA

gi|215721|gb|M24870|PQBNVWSIB [215721]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )

M24869

Bacteriophage Q-beta nanovariant WSI RNA

gi|215720|gb|M24869|PQBNVWSIA [215720]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )

M10495

Coliphage Q-beta MDV-1(+) RNA

gi|215719|gb|M10495|PQBMDV1A [215719]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 10 nucleotide neighbors )

J02484

bacteriophage qbeta coat protein cistron first half

gi|215717|gb|J02484|PQBCP5 [215717]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

M57754

Bacteriophage Q-beta minus strand RNA, 5' terminus

gi|215716|gb|M57754|PQBBMS5E [215716]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 8 nucleotide neighbors )

M24297

Bacteriophage Q-beta 5'-terminal region of the minus strand

gi|215715|gb|M24297|PQB5END [215715]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 8 nucleotide neighbors )

## M10695

Bacteriophage Q-beta, MDV-1 RNA

gi|215714|gb|M10695|PQB1IR [215714]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 12 nucleotide neighbors )

## M24827

Bacteriophage R17 A protein gene, 5' end

gi|216078|gb|M24827|R17RNACIS [216078]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors )

## M24829

Bacteriophage R17 coat protein gene, 5' end

gi|216075|gb|M24829|R17CP5 [216075]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors )

## J02488

bacteriophage r17 rna synthetase initiation site

gi|216080|gb|J02488|R17RNASYN [216080]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 2 protein links, or 6 nucleotide neighbors )

## J02487

bacteriophage r17 coat protein initiation site

gi|216073|gb|J02487|R17COATP [216073]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## J02486

bacteriophage r17 a protein initiation site

gi|216071|gb|J02486|R17APROT [216071]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## M24826

Bacteriophage R17 coat protein RNA fragment

gi|216077|gb|M24826|R17CPRAA [216077]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 7 nucleotide neighbors )

## M24296

Bacteriophage R17 3'-terminal fragment A RNA

gi|216070|gb|M24296|R173TFA [216070]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 9 nucleotide neighbors )

## 1TFN

structure refinement for a 24-nucleotide rna hairpin, nmr, minimized average

structure ribonucleic acid, hairpin, bacteriophage r17 mol\_id: 1; molecule: r17c; chain: null; engineered: yes

gi|1942336|pdb|1TFN| [1942336]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 structure link )

## 1RPEA

rna (5'-d(gpgpgpapcpupgpgpapcpupcpapcpup cpapgpupcpupapu-3') (24-mer rna

hairpin coat protein binding site for bacteriophage r17) (nmr, minimized average structure)

gi|1421020|pdb|1RHT| [1421020]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 structure link )

M14428

Bacteriophage S13 circular DNA, complete genome

gi|216089|gb|M14428|S13CG [216089]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 12 protein links, 26 nucleotide neighbors, or 1 genome link )

J05393

Bacteriophage T1 DNA N-6-adenine-methyltransferase (M.T1) gene, complete cds

gi|166163|gb|J05393|BT1NAMTA [166163]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links )

L46845

Bacteriophage T2 frd3, frd2 genes, complete cds

gi|951387|gb|L46845|PT2FRD32G [951387]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 17 nucleotide neighbors )

L43611

Bacteriophage T2 fibritin (wac) gene, complete cds

gi|903869|gb|L43611|PT2WAC [903869]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 4 nucleotide neighbors )

M24812

Bacteriophage T2 secondary structure RNA sequence

gi|215796|gb|M24812|PT2RNA [215796]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 nucleotide neighbors )

M22342

Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds

gi|215792|gb|M22342|PT2DAM [215792]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors )

S57515

orf 61.2 {intergenic region between 41 and 61} [bacteriophage T2, Genomic, 323 nt]

gi|298524|gb|S57515|S57515 [298524]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

X05312

Bacteriophage T2 gene 38 for receptor recognizing protein

gi|15197|emb|X05312|MYT2G38 [15197]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

X04442

Bacteriophage T2 gene 37 for receptor recognizing protein

gi|15195|emb|X04442|MYT2G37 [15195]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

X12460

Bacteriophage T2 gene 32 mRNA for single-stranded DNA binding protein

gi|15192|emb|X12460|MYT2G32 [15192]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 14 nucleotide neighbors )

X57797

Bacteriophage T2 gene for gp12

gi|14875|emb|X56555|BT2GP12 [14875]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 2 nucleotide neighbors )

## X01755

Bacteriophage T2 tail fiber gene 36

gi|15189|emb|X01755|MYT2F36 [15189]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

## M14784

Bacteriophage T3 strain amNG220B right end, tail fiber protein, lysis protein and DNA packaging proteins, complete cds

gi|215810|gb|M14784|PT3RE [215810]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, or 10 nucleotide neighbors )

## SEG\_PT3RNAPOL

Bacteriophage T3 RNA polymerase III gene, 5' end

gi|710559|gb|SEG\_PT3RNAPOL [710559]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

## M22610

Bacteriophage T3 RNA polymerase III gene, 3' end

gi|340722|gb|M22610|PT3RNAPOL2 [340722]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## M22609

Bacteriophage T3 RNA polymerase III gene, 5' end

gi|340721|gb|M22609|PT3RNAPOL1 [340721]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## X05031

Bacteriophage T3 gene region 1-2.5 with primary origin of replication

gi|15719|emb|X05031|POT3ORI [15719]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 11 protein links, or 5 nucleotide neighbors )

## X03964

Bacteriophage T3 early control region pos. 308-810 from genome left end

gi|15718|emb|X03964|POT3EP [15718]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 20 nucleotide neighbors )

## X17255

Bacteriophage T3 gene 1 to gene 11

gi|15682|emb|X17255|POT3111G [15682]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 MEDLINE links, 36 protein links, 17 nucleotide neighbors, or 1 genome link )

## X15840

Phage T3 gene 10

gi|15625|emb|X15840|PODT3G10 [15625]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors )

## X02981

Bacteriophage T3 gene 1 for RNA polymerase

gi|15561|emb|X02981|PODOT3P [15561]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

## J02503

bacteriophage t3 5' end, terminally redundant sequence (trs)

gi|215816|gb|J02503|PT3TRS1 [215816]

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## SEG\_PT3TRS

bacteriophage t3 5' end, terminally redundant sequence (trs)

gi|215818|gb|SEG\_PT3TRS [215818]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## J02504

bacteriophage t3 3' end, terminally redundant sequence (trs)

gi|215817|gb|J02504|PT3TRS2 [215817]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

HYPERLINK <http://www.rs.noda.sut.ac.jp/~kunisawa> <http://www.rs.noda.sut.ac.jp/~kunisawa>

Bacteriophage T4 genomic database compiled by Arisaka et al.

## X95646

Bacteriophage T5 DNA for region 60.5%-71% of the T5 genome

gi|2791557|emb|AJ001191|BTJ001191 [2791557]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,7 MEDLINE links, 12 protein links, or 6 nucleotide neighbors )

## X56847

Bacteriophage T5 genomic region encoding early genes D10-D15

gi|15407|emb|X12930|MYT5D10 [15407]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 5 protein links, or 4 nucleotide neighbors )

## AF039886

Bacteriophage T5 subclone T5.5.3r5.18r, single pass sequence, genomic survey sequence

gi|2811154|gb|AF039886|AF039886 [2811154]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039885

Bacteriophage T5 subclone T5.40f,41f, single pass sequence, genomic survey sequence

gi|2811153|gb|AF039885|AF039885 [2811153]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039884

Bacteriophage T5 subclone T5.26.fr, single pass sequence, genomic survey sequence

gi|2811152|gb|AF039884|AF039884 [2811152]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039883

Bacteriophage T5 subclone 10-T5.5.7F, single pass sequence, genomic survey sequence

gi|2811151|gb|AF039883|AF039883 [2811151]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039882

Bacteriophage T5 subclone 41-T5.5.4BF, single pass sequence, genomic survey sequence

gi|2811150|gb|AF039882|AF039882 [2811150]

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## AF039881

Bacteriophage T5 subclone 39-T5.5.4aF, single pass sequence, genomic survey sequence

gi|2811149|gb|AF039881|AF039881 [2811149]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor )

## AF039880

Bacteriophage T5 subclone 19-T5.7.2r, single pass sequence, genomic survey sequence  
 gi|2811148|gb|AF039880|AF039880 [2811148]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039879

Bacteriophage T5 subclone 18-T5.7.2F, single pass sequence, genomic survey sequence  
 gi|2811147|gb|AF039879|AF039879 [2811147]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039878

Bacteriophage T5 subclone 11-T5.5.7R, single pass sequence, genomic survey sequence  
 gi|2811146|gb|AF039878|AF039878 [2811146]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 nucleotide neighbors )

## AF039877

Bacteriophage T5 subclone T5.4FR, single pass sequence, genomic survey sequence  
 gi|2811145|gb|AF039877|AF039877 [2811145]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039876

Bacteriophage T5 subclone 22-T5.16R, single pass sequence, genomic survey sequence  
 gi|2811144|gb|AF039876|AF039876 [2811144]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039875

Bacteriophage T5 subclone 21-T5.16R, single pass sequence, genomic survey sequence  
 gi|2811143|gb|AF039875|AF039875 [2811143]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039874

Bacteriophage T5 subclone 21-T5.16F, single pass sequence, genomic survey sequence  
 gi|2811142|gb|AF039874|AF039874 [2811142]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039873

Bacteriophage T5 subclone 09-T5.6F, single pass sequence, genomic survey sequence  
 gi|2811141|gb|AF039873|AF039873 [2811141]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039872

Bacteriophage T5 subclone 09-T5.6R, single pass sequence, genomic survey sequence  
 gi|2811140|gb|AF039872|AF039872 [2811140]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 nucleotide neighbors )

## AF039871

Bacteriophage T5 subclone 04-T5.26.R, single pass sequence, genomic survey sequence  
 gi|2811139|gb|AF039871|AF039871 [2811139]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF039870

Bacteriophage T5 subclone 13-T5.42F, single pass sequence, genomic survey sequence  
 gi|2811138|gb|AF039870|AF039870 [2811138]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## X69460

Bacteriophage T5 ltf gene for L-shaped tail fibers

gi|15415|emb|X69460|MYT5LTF [15415]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 1 protein link, or 4 nucleotide neighbors )

## X03402

Bacteriophage T5 D15 gene for 5' exonuclease

gi|15413|emb|X03402|MYT5EXOG [15413]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors )

## Z11972

Bacteriophage T5 tRNA-Tyr, tRNA-Glu, tRNA-Trp, tRNA-Phe, tRNA-Cys and  
tRNA-Asn genes, and ORFs 91aa, 90aa, 42aa and 172aa

gi|15795|emb|Z11972|T56TRNAG [15795]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 3 nucleotide neighbors )

## X03898

Bacteriophage T5 genes for tRNA-His, -Ser and -Leu

gi|15786|emb|X03898|STT5RN1 [15786]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 MEDLINE links )

## X04177

Bacteriophage T5 gene for transfer RNA-Gln

gi|15421|emb|X04177|MYT5TRNQ [15421]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )

## X03899

Bacteriophage T5 genes for tRNA-Val, -Lys, -fMet, -Pro and -Ile3

gi|15787|emb|X03899|STT5RN2 [15787]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## X03798

Bacteriophage T5 gene for tRNA-Asp (GUC)

gi|15472|emb|X03798|NCT5TRDG [15472]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

## Y00364

Bacteriophage T5 tRNA gene cluster (27.8%-22.4%)

gi|15420|emb|Y00364|MYT5TRN [15420]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors )

## X03140

Bacteriophage T5 DNA with rho-dependent transcription terminator (Hind III-P fragment)

gi|15417|emb|X03140|MYT5RHO [15417]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

## Z35070

Bacteriophage T6 DNA

gi|535228|emb|Z35074|MYEREGBT6 [535228]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )



## AF060870

Coliphage T6 small subunit distal tail fiber (gene 36) gene, partial cds; and large subunit distal tail fiber (gene 37) and tail fiber adhesin (gene 38) genes, complete cds

gi|3676458|gb|AF052605|AF052605 [3676458]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 protein links, or 2 nucleotide neighbors )

## Z35072

Bacteriophage T6 DNA encoding ORF19.1 gene and g19 gene

gi|535232|emb|Z35072|MYTAILT6 [535232]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links )

## X12488

Bacteriophage T6 gene 32 mRNA for single-stranded DNA binding protein

gi|15843|emb|X12488|MYT6G32 [15843]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 14 nucleotide neighbors )

## Z78095

Bacteriophage T6 DNA (1506 bp)

gi|1488562|emb|Z78095|BPHZ78095 [1488562]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 4 nucleotide neighbors )

## Z35079

Bacteriophage T6 DNA for Ip5, Ip6

gi|535215|emb|Z35079|MY57BT6 [535215]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

## X68725

E.coli bacteriophage T6 gene for beta-glucosyl-HMC-alpha-glucosyl-transferase

gi|296439|emb|X68725|ECT6 [296439]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

## X69894

Bacteriophage T6 alt gene for ADP-Ribosyltransferase

gi|15422|emb|X69894|MYT6ADP [15422]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## L46846

Bacteriophage T6 frd3, frd2 genes, complete cds

gi|951390|gb|L46846|PT6FRD32G [951390]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links )

## M27738

Bacteriophage T6 translational repressor protein (regA), complete cds

gi|215993|gb|M27738|PT6REGA [215993]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 5 nucleotide neighbors )

## M38465

Bacteriophage T6 DNA ligase gene, complete cds

gi|215991|gb|M38465|PT6LIG55 [215991]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors )

V01146

Genome of bacteriophage T7

gi|431187|emb|V01146|T7CG [431187]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,13 MEDLINE links, 60 protein links, 105 nucleotide neighbors, or 1 genome link )

X60322

Bacteriophage alpha3 genes A, B, K, C, D, E, J, F, G, H

gi|14775|emb|X60322|BACALPHA [14775]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 10 protein links, 22 nucleotide neighbors, or 1 genome link )

X13332

Bacteriophage alpha3 DNA for origin of replication

gi|15093|emb|X13332|MIA3ORPL [15093]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

X12611

Bacteriophage alpha3 gene for protein A part., finger domain

gi|15092|emb|X12611|MIA3AFIN [15092]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 6 nucleotide neighbors )

X15721

Bacteriophage alpha3 deletion mutation DNA for the origin region (-ori) of replication

gi|14774|emb|X15721|BA3DMOR9 [14774]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors )

X15720

Bacteriophage alpha3 deletion mutant DNA for the origin region (-ori) of replication

gi|14773|emb|X15720|BA3DMOR8 [14773]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

X15719

Bacteriophage alpha3 insertion mutant DNA for the origin region (-ori) of replication

gi|14772|emb|X15719|BA3DMOR7 [14772]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 10 nucleotide neighbors )

X15718

Bacteriophage alpha3 deletion mutation DNA for origin region (-ori) of replication

gi|14771|emb|X15718|BA3DMOR6 [14771]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors )

X15717

Bacteriophage alpha3 deletion mutant DNA for origin region (-ori) of replication

gi|14770|emb|X15717|BA3DMOR5 [14770]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 9 nucleotide neighbors )

X15716

Bacteriophage alpha3 deletion mutant DNA for origin region (-ori) of replication

gi|14769|emb|X15716|BA3DMOR4 [14769]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 10 nucleotide neighbors )

## X15715

Bacteriophage alpha3 deletion mutant DNA for origin region (-ori) of replication

gi|14768|emb|X15715|BA3DMOR3 [14768]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors )

## X15714

Bacteriophage alpha3 deletion mutant DNA for origin region (-ori) of replication

gi|14767|emb|X15714|BA3DMOR2 [14767]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors )

## X15713

Bacteriophage alpha3 deletion mutant DNA for the origin region (-ori) of replication

gi|14766|emb|X15713|BA3DMOR1 [14766]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 11 nucleotide neighbors )

## X62059

Bacteriophage alpha3 origin of cDNA synthesis (oriGA)

gi|14763|emb|X62059|AL3ORIGA [14763]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors )

## X62058

Bacteriophage alpha3 origin of cDNA synthesis (oriAA)

gi|14762|emb|X62058|AL3ORIAA [14762]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 nucleotide neighbors )

## J02444

Bacteriophage alpha3 origin of DNA replication

gi|166103|gb|J02444|AL3ORI [166103]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 12 nucleotide neighbors )

## M25640

Bacteriophage alpha-3 H protein gene, complete cds

gi|166101|gb|M25640|AL3HP [166101]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 13 nucleotide neighbors )

## M10631

Bacteriophage alpha-3 cleavage site for phage phi-X174 gene A protein

gi|166099|gb|M10631|AL3CSA [166099]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

## X00774

Bacteriophage alpha-3 gene J sequence

gi|15431|emb|X00774|NCBA3J [15431]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 2 nucleotide neighbors )

## M25640

Bacteriophage alpha-3 H protein gene, complete cds

gi|166101|gb|M25640|AL3HP [166101]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 13 nucleotide neighbors )

## M10631

Bacteriophage alpha-3 cleavage site for phage phi-X174 gene A protein

gi|166099|gb|M10631|AL3CSA [166099]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

## J02459

Bacteriophage lambda, complete genome

gi|215104|gb|J02459|LAMCG [215104]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,87 MEDLINE links, 67 protein links, 190 nucleotide neighbors, or 1 genome link )

## J02482

Bacteriophage phi-X174, complete genome

gi|216019|gb|J02482|PX1CG [216019]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,23 MEDLINE links, 11 protein links, 26 nucleotide neighbors, or 1 genome link )

## J02454

Bacteriophage G4, complete genome

gi|215415|gb|J02454|PG4CG [215415]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 11 protein links, 20 nucleotide neighbors, or 1 genome link )

## X60323

Bacteriophage phiK complete genome

gi|1478118|emb|X60323|BPHIKCG [1478118]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,10 protein links, 18 nucleotide neighbors, or 1 genome link )

## L42820

Bacteriophage BF23 tail protein (hrs) gene, complete cds

gi|1048680|gb|L42820|BBFHRS [1048680]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## X54455

Bacteriophage BF23 gene 17 and gene 18

gi|14797|emb|X54455|BF231718G [14797]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 2 nucleotide neighbors )

## M37097

Bacteriophage BF23 DNA, right end of terminal repetition

gi|166115|gb|M37097|BBFRIGH [166115]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )

## M37096

Bacteriophage BF23 DNA, left end of terminal repetition

gi|166114|gb|M37096|BBFLEFT [166114]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

## M37095

Bacteriophage BF23 A2-A3 gene, complete cds, and A1 gene, 5' end

gi|166110|gb|M37095|BBFA2A3 [166110]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 3 protein links, or 1 nucleotide neighbor )

## AF056281

Bacteriophage BF23 clone bf23.mac5/6.1, genomic survey sequence

gi|3090930|gb|AF056281|AF056281 [3090930]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056280

Bacteriophage BF23 clone bf23.mac3, genomic survey sequence  
gi|3090929|gb|AF056280|AF056280 [3090929]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056279

Bacteriophage BF23 clone bf23.mac18/21.34, genomic survey sequence  
gi|3090928|gb|AF056279|AF056279 [3090928]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056278

Bacteriophage BF23 clone bf23.mac16/19.33, genomic survey sequence  
gi|3090927|gb|AF056278|AF056278 [3090927]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056277

Bacteriophage BF23 clone bf23.mac16/19-33, genomic survey sequence  
gi|3090926|gb|AF056277|AF056277 [3090926]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056276

Bacteriophage BF23 clone bf23.mac12/9-9, genomic survey sequence  
gi|3090925|gb|AF056276|AF056276 [3090925]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056275

Bacteriophage BF23 clone bf23.mac11/14-24, genomic survey sequence  
gi|3090924|gb|AF056275|AF056275 [3090924]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056274

Bacteriophage BF23 clone bf23.57r64r, genomic survey sequence  
gi|3090923|gb|AF056274|AF056274 [3090923]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 3 nucleotide neighbors )

AF056273

Bacteriophage BF23 clone bf23.54fr, genomic survey sequence  
gi|3090922|gb|AF056273|AF056273 [3090922]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056272

Bacteriophage BF23 clone bf23.47fr.mac10/7, genomic survey sequence  
gi|3090921|gb|AF056272|AF056272 [3090921]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056271

Bacteriophage BF23 clone bf23.23.66r, genomic survey sequence  
gi|3090920|gb|AF056271|AF056271 [3090920]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

AF056270

Bacteriophage BF23 clone bf23.23.64f, genomic survey sequence  
gi|3090919|gb|AF056270|AF056270 [3090919]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056269

Bacteriophage BF23 clone bf23.23.60r, genomic survey sequence  
 gi|3090918|gb|AF056269|AF056269 [3090918]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056268

Bacteriophage BF23 clone bf23.23.60f, genomic survey sequence  
 gi|3090917|gb|AF056268|AF056268 [3090917]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor )

## AF056267

Bacteriophage BF23 clone bf23.23.59r, genomic survey sequence  
 gi|3090916|gb|AF056267|AF056267 [3090916]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056266

Bacteriophage BF23 clone bf23.23.59f, genomic survey sequence  
 gi|3090915|gb|AF056266|AF056266 [3090915]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056265

Bacteriophage BF23 clone bf23.23.56r, genomic survey sequence  
 gi|3090914|gb|AF056265|AF056265 [3090914]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056264

Bacteriophage BF23 clone bf23.23.56f, genomic survey sequence  
 gi|3090913|gb|AF056264|AF056264 [3090913]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056263

Bacteriophage BF23 clone bf23.23.68f55r, genomic survey sequence  
 gi|3090912|gb|AF056263|AF056263 [3090912]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056262

Bacteriophage BF23 clone bf23.23.43fr.66f, genomic survey sequence  
 gi|3090911|gb|AF056262|AF056262 [3090911]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056261

Bacteriophage BF23 clone bf23.23.2fr, genomic survey sequence  
 gi|3090910|gb|AF056261|AF056261 [3090910]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056260

Bacteriophage BF23 clone bf23.23.55.f, genomic survey sequence  
 gi|3090909|gb|AF056260|AF056260 [3090909]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056259

Bacteriophage BF23 clone bf23.23.53.r, genomic survey sequence  
 gi|3090908|gb|AF056259|AF056259 [3090908]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056258

Bacteriophage BF23 clone bf23.23.53.f, genomic survey sequence  
gi|3090907|gb|AF056258|AF056258 [3090907]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056257

Bacteriophage BF23 clone bf23.23.52.r, genomic survey sequence  
gi|3090906|gb|AF056257|AF056257 [3090906]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056256

Bacteriophage BF23 clone bf23.23.52.f, genomic survey sequence  
gi|3090905|gb|AF056256|AF056256 [3090905]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056255

Bacteriophage BF23 clone bf23.23.49.r, genomic survey sequence  
gi|3090904|gb|AF056255|AF056255 [3090904]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056254

Bacteriophage BF23 clone bf23.23.49.f, genomic survey sequence  
gi|3090903|gb|AF056254|AF056254 [3090903]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056253

Bacteriophage BF23 clone bf23.23.48.r, genomic survey sequence  
gi|3090902|gb|AF056253|AF056253 [3090902]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056252

Bacteriophage BF23 clone bf23.23.48.f, genomic survey sequence  
gi|3090901|gb|AF056252|AF056252 [3090901]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056251

Bacteriophage BF23 clone bf23.23.44.r, genomic survey sequence  
gi|3090900|gb|AF056251|AF056251 [3090900]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056250

Bacteriophage BF23 clone bf23.23.41.f, genomic survey sequence  
gi|3090899|gb|AF056250|AF056250 [3090899]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056249

Bacteriophage BF23 clone bf23.23.22.a.r, genomic survey sequence  
gi|3090898|gb|AF056249|AF056249 [3090898]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056248

Bacteriophage BF23 clone bf23.23.22.a.f, genomic survey sequence  
gi|3090897|gb|AF056248|AF056248 [3090897]  
(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## AF056247

Bacteriophage BF23 clone bf23.23.68.r, genomic survey sequence  
 gi|3090896|gb|AF056247|AF056247 [3090896]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## Z50114

Bacteriophage BF23 DNA for putative tail protein gene  
 gi|2464952|emb|Z50114|BF23LATE [2464952]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link )

## D12824

Bacteriophage BF23 genes for minor tail protein gp24 and major tail protein gp25, complete cds  
 gi|520578|dbj|D12824|BBF2TAIL [520578]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors )

## Z34953

Bacteriophage K3 ip9, ip7 and ip8 genes  
 gi|535261|emb|Z34953|MYK3IP978 [535261]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

## Z35075

Bacteriophage K3 DNA for Ip3 and Ip4  
 gi|535229|emb|Z35075|MYEORF64K [535229]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links )

## X05560

Bacteriophage K3 gene 38 for receptor recognizing protein  
 gi|15112|emb|X05560|MYK3G38 [15112]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

## X04747

Bacteriophage K3 gene 37 for receptor recognizing protein  
 gi|15110|emb|X04747|MYK3G37 [15110]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors )

## X01754

Bacteriophage K3 tail fiber gene 36  
 gi|15108|emb|X01754|MYK3F36 [15108]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links )

## M16812

Bacteriophage K3 't' lysis gene, complete cds  
 gi|215503|gb|M16812|PK3LYST [215503]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

## L46833

Bacteriophage K3 frd3, frd2 genes, complete cds  
 gi|951377|gb|L46833|PK3FRD32G [951377]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 2 nucleotide neighbors )

## L43613

Bacteriophage K3 fibrin (wac) gene, complete cds  
 gi|903861|gb|L43613|PK3WAC [903861]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 4 nucleotide neighbors )



## X01753

Bacteriophage Ox2 tail fiber gene 36

gi|15122|emb|X01753|MYOX2F36 [15122]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

## L43612

Bacteriophage Ox2 fibrin (wac) gene, complete cds

gi|903848|gb|L43612|OX2WAC [903848]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 4 nucleotide neighbors )

## Z46880

Bacteriophage OX2 stp gene

gi|599663|emb|Z46880|BPOX2STP [599663]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

## X05675

Bacteriophage Ox2 gene 38 for receptor-recognizing protein and flanking regions

gi|15124|emb|X05675|MYOX2G38 [15124]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

## M33533

Bacteriophage RB18 translational repressor protein (regA) and Orf43.1, complete cds

gi|216083|gb|M33533|RB18REGA [216083]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

## AF033329

Bacteriophage RB18 single-stranded binding protein (gene 32) gene, partial cds, and 5' region

gi|2645788|gb|AF033329|AF033329 [2645788]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 11 nucleotide neighbors )

## M86231

Bacteriophage RB69 gene 62, 3'end; RegA (regA) gene, complete cds

gi|215354|gb|M86231|P6962REGA [215354]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

## AF033332

Bacteriophage RB69 single-stranded binding protein (gene 32) gene, partial cds, and 5' region

gi|2645794|gb|AF033332|AF033332 [2645794]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 12 nucleotide neighbors )

## U34036

Bacteriophage RB69 DNA polymerase (43) gene, complete cds

gi|1237125|gb|U34036|BRU34036 [1237125]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

## V01145

Bacteriophage H1 genome fragment Each Thymine given in this sequence represents a HMU-residue  
(HMU = 5-hydroxymethyluracil)

gi|15557|emb|V01145|PODOH1 [15557]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## X05676

Bacteriophage M1 gene 38 for receptor recognizing protein and flanking regions

gi|15114|emb|X05676|MYM1G38 [15114]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

## AF034575

Bacteriophage M1 putative integrase (int) gene, complete cds, and attP region, complete sequence  
gi|2662472|gb|AF034575|AF034575 [2662472]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

## AF033321

Bacteriophage M1 single-stranded binding protein (gene 32) gene, partial cds, and 5' region  
gi|2645772|gb|AF033321|AF033321 [2645772]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 17 nucleotide neighbors )

## X55190

Bacteriophage Tu1a 37 and 38 genes for receptor-recognizing proteins 37 and 38 (respectively), partial cds  
gi|14860|emb|X55190|BPTUIA [14860]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

## AF033334

Bacteriophage Tu1b single-stranded binding protein (gene 32) gene, partial cds, and 5' region  
gi|2645798|gb|AF033334|AF033334 [2645798]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 5 nucleotide neighbors )

## X55191

Bacteriophage Tu1b 37 gene for receptor-recognizing protein 37 (partial cds), 38 gene for receptor-recognizing protein 38, and t gene (partial cds)

gi|14863|emb|X55191|BPTUIB [14863]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 3 nucleotide neighbors )

## X13065

Bacteriophage phi80 early region

gi|14800|emb|X13065|BP80ER [14800]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 8 protein links, or 6 nucleotide neighbors )

## D00360

Bacteriophage phi80 cor gene

gi|217782|dbj|D00360|P8080COR [217782]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link )

## X01639

Bacteriophage phi 80 DNA-fragment with replication origin

gi|15828|emb|X01639|XXPHI80 [15828]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 25 nucleotide neighbors )

## X04051

Lambdoid bacteriophage phi 80 int-xis region (integrase-excisionase region)

gi|15770|emb|X04051|STPHI80X [15770]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

## X06751

Phage Phi80 DNA for major coat protein

gi|15768|emb|X06751|STPHI80C [15768]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 11 nucleotide neighbors )

## X75949

Bacteriophage phi80 DNA for ORF x171.8 and ORF x171.28'

gi|458811|emb|X75949|ECORF171B [458811]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 28 nucleotide neighbors )

L40418

Bacteriophage phi-80 gene, complete cds

gi|1019107|gb|L40418|P80A [1019107]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

M24831

Bacteriophage phi-80 Tyr-tRNA gene, 3' end

gi|215363|gb|M24831|P80TGY [215363]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 43 nucleotide neighbors )

M10670

Bacteriophage phi-80 replication origin

gi|215361|gb|M10670|P80ORI [215361]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

M24825

Bacteriophage phi-80 RNA fragment

gi|215360|gb|M24825|P80M3A [215360]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

M11919

Bacteriophage phi-80 cI immunity region encoding the N gene

gi|215358|gb|M11919|P80CI [215358]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors )

M10891

Bacteriophage phi-80 attP site DNA

gi|215357|gb|M10891|P80ATTP [215357]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 nucleotide neighbor )

M19473

Bacteriophage 933J (from E.coli) proviral Shiga-like toxin type 1 subunits A and B genes, complete cds

gi|215072|gb|M19473|J93SLTI [215072]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 2 protein links, or 20 nucleotide neighbors )

Y10775

Bacteriophage 933W ileX, stx2A and stx2B genes

gi|1938206|emb|Y10775|BP933ILEX [1938206]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 36 nucleotide neighbors )

X83722

Bacteriophage 933W slt-IIB gene

gi|1490229|emb|X83722|B933WSLT [1490229]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 20 nucleotide neighbors )

X07865

Bacteriophage 933W slt-II gene for Shiga-like toxin typeII subunit A and B

gi|14892|emb|X07865|BWSLTII [14892]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 29 nucleotide neighbors )

M16625

Bacteriophage H19B (from E.coli) sltIA and sltIB genes encoding Shiga-like toxin I subunits A and B, complete cds

gi|215043|gb|M16625|H19BSLT [215043]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 24 nucleotide neighbors )

## M17358

Bacteriophage H19B shiga-like toxin-1 (SLT-1) A and B subunit DNA, complete cds

gi|215046|gb|M17358|H19BSLTA [215046]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 20 nucleotide neighbors )

## U29728

Bacteriophage N4 single-stranded DNA-binding protein (N4SSB) gene, complete cds

gi|939708|gb|U29728|BNU29728 [939708]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 1 protein link )

## J02580

Bacteriophage PA-2 (E.coli porcine strain isolate) Rz gene, 5'end; ORF2, outer membrane porin protein (lc) and ORF1 genes, complete cds

gi|215366|gb|J02580|PA2LC [215366]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 4 nucleotide neighbors )

## U32222

Bacteriophage 186, complete sequence

gi|3337249|gb|U32222|B1U32222 [3337249]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 46 protein links, or 5 nucleotide neighbors )

## X51522

Bacteriophage P4 complete DNA genome

gi|450916|emb|X51522|MYP4CG [450916]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 13 protein links, 6 nucleotide neighbors, or 1 genome link )

## X92588

Bacteriophage 82 orf33, orf151, orf56, orf96, rus, orf45, and Q genes

gi|1051111|emb|X92588|BAC82HOLL [1051111]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,7 protein links, or 1 nucleotide neighbor )

## J02803

Bacteriophage 82 antitermination protein (Q) gene, complete cds

gi|215364|gb|J02803|P82Q [215364]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

## U02466

Bacteriophage HK022 (cro), (cII) and (O) genes, complete cds, (P) gene, partial cds

gi|407285|gb|U02466|BHU02466 [407285]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 5 protein links, or 1 nucleotide neighbor )

## M26291

Bacteriophage D108 regulatory DNA-binding protein (ner) gene, complete cds

gi|166194|gb|M26291|D18NER [166194]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## M11272

Bacteriophage D108 left-end DNA

gi|166193|gb|M11272|D18LEDNA [166193]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 nucleotide neighbors )

## M18902

Bacteriophage D108 kil gene encoding a replication protein, 3' end; and containing three ORFs, complete cds

gi|166191|gb|M18902|D18KIL [166191]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

## M10191

Bacteriophage D108, left end with Mu A protein binding sites L1 and L2

gi|166190|gb|M10191|D18BSL [166190]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors )

## J02447

bacteriophage d108 gene a 5' end

gi|166189|gb|J02447|D18AAA [166189]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## V00865

Bacteriophage D108 fragment from genes A and ner (C-terminus of ner and N-terminus of A)

gi|15437|emb|V00865|NCD108 [15437]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links )

## X01914

Bacteriophage IKe gene for DNA binding protein

gi|14957|emb|X01914|INIKEDBP [14957]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors )

## AF064539

Bacteriophage N15, complete genome

gi|3192683|gb|AF064539|AF064539 [3192683]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 60 protein links, 26 nucleotide neighbors, or 1 genome link )

## U02303

Bacteriophage If1, complete genome

gi|3676280|gb|U02303|B2U02303 [3676280]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,10 protein links, or 1 genome link )

## AF007792

Bacteriophage Mu late morphogenetic region

gi|3551775|gb|AF007792|AF007792 [3551775]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor )

## U24159

Bacteriophage HP1 strain HP1c1, complete genome

gi|1046235|gb|U24159|BHU24159 [1046235]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 41 protein links, 8 nucleotide neighbors, or 1 genome link )

## Z71579

Bacteriophage S2 type A 5.6 kb DNA fragment

gi|1679806|emb|Z71579|BPHS1ADNA [1679806]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 9 protein links, or 9 nucleotide neighbors )

## X53238

Klebsiella sp. bacteriophage K11 gene 1 for RNA polymerase

gi|14984|emb|X53238|KSK11RPO [14984]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## X85010

Bacteriophage A511 ply511 gene

gi|853748|emb|X85010|BPA511PLY [853748]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

## U29728

Bacteriophage N4 single-stranded DNA-binding protein (N4SSB) gene, complete cds

gi|939708|gb|U29728|BNU29728 [939708]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 1 protein link )

## J02445

bacteriophage bo1 3'-terminal region rna

gi|166152|gb|J02445|BO1TR3 [166152]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 5 nucleotide neighbors )

## L06183

Bacteriophage L5 (from *Leuconostoc oenos*) genome

gi|289353|gb|L06183|BL5GENM [289353]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 genome link )

## AF074945

*Mycoplasma arthritidis* bacteriophage MAV1, complete genome

gi|3511243|gb|AF074945|AF074945 [3511243]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,15 protein links, 3 nucleotide neighbors, or 1 genome link )

## L13696

Bacteriophage L2 (from *Mycoplasma*), complete genome

gi|289338|gb|L13696|BL2CG [289338]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 14 protein links, or 1 genome link )

## X80191

Bacteriophage PP7 mRNA for maturation, coat, lysis and replicase proteins

gi|517237|emb|X80191|BPP7PR [517237]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 1 genome link )

## M19377

Bacteriophage Pf3 from *Pseudomonas aeruginosa* (New York strain), complete genome

gi|215380|gb|M19377|PF3COMNY [215380]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, or 5 nucleotide neighbors )

## M11912

Bacteriophage Pf3 from *Pseudomonas aeruginosa* (Nijmegen strain), complete genome

gi|215371|gb|M11912|PF3COMN [215371]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, 5 nucleotide neighbors, or 1 genome link )

## V00605

Bacteriophage Pf1 gene encoding DNA binding protein

gi|14970|emb|V00605|INOPF1 [14970]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 1 nucleotide neighbor )

## L05626

Bacteriophage PR4 capsid protein (P6) gene, complete cds

gi|215735|gb|L05626|PR4P6MAJA [215735]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## D13409

Bacteriophage phiCTX (isolated from *Pseudomonas aeruginosa*) cosR, attP, int genes

gi|217776|dbj|D13409|BPHCOSR [217776]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 3 nucleotide neighbors )

## D13408

Bacteriophage phiCTX (isolated from *Pseudomonas aeruginosa*) cosL, ctx genes

gi|217775|dbj|D13408|BPHCOSLCTX [217775]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 3 nucleotide neighbors )

## M24832

Bacteriophage f2 coat protein gene, partial cds

gi|166228|gb|M24832|F2CRNACA [166228]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

## S72011

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes,partial cds

gi|2618967|gb|AF017629|AF017629 [2618967]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors )

## AF017628

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618964|gb|AF017628|AF017628 [2618964]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors )

## AF017627

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618961|gb|AF017627|AF017627 [2618961]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors )

## AF017626

Bacteriophage 21 isocitrate dehydrogenase (icd) gene, partial cds; and integrase (int) gene, partial cds

gi|2618958|gb|AF017626|AF017626 [2618958]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 49 nucleotide neighbors )

## AF017625

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618955|gb|AF017625|AF017625 [2618955]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors )

## AF017624

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int)genes, partial cds

gi|2618952|gb|AF017624|AF017624 [2618952]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 44 nucleotide neighbors )

## AF017623

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618949|gb|AF017623|AF017623 [2618949]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017622

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618946|gb|AF017622|AF017622 [2618946]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017621

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618943|gb|AF017621|AF017621 [2618943]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## D26449

Bacteriophage PS17 FI gene for tail sheath protein (gpFI) and FII gene for tail tube protein (gpFII), complete cds

gi|452162|dbj|D26449|BPSFIFII [452162]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links )

## X87627

Bacteriophage D3112 A and B genes

gi|974768|emb|X87627|BPD3112AB [974768]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 2 protein links, or 1 nucleotide neighbor )

## U32623

Bacteriophage D3 transcriptional activator CII (cII) gene, complete cds

gi|984852|gb|U32623|BDU32623 [984852]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 1 nucleotide neighbor )

## L34781

Bacteriophage phi 11 holin homologue (ORF3) gene, complete cds and peptidoglycan hydrolase (lytA) gene, partial cds

gi|511838|gb|L34781|BPHHOLIN [511838]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 2 nucleotide neighbors )

## L14810

Bacteriophage P22 (gp10) gene, complete cds, and (gp26) gene, complete cds

gi|294053|gb|L14810|P22GP1026X [294053]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

## X87420

Bacteriophage ES18 genes 24, c2, cro, c1, 18, and oL and oR operators

gi|1143407|emb|X87420|BPES18GEN [1143407]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 protein links, or 9 nucleotide neighbors )

## L42820

Bacteriophage BF23 tail protein (hrs) gene, complete cds

gi|1048680|gb|L42820|BBFHRS [1048680]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 1 protein link, or 1 nucleotide neighbor )

## X14980

Bacteriophage PRD1 XV gene for protein P15 (lytic enzyme)

gi|15802|emb|X14980|TEPRD1XV [15802]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 1 protein link, or 4 nucleotide neighbors )

## X06321

Bacteriophage PRD1 gene 8 for DNA terminal protein

gi|15800|emb|X06321|TEPRD18 [15800]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 10 nucleotide neighbors )

## X14336

Filamentous Bacteriophage I2-2 genome

gi|14920|emb|X14336|INBI22 [14920]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, 1 nucleotide neighbor, or 1 genome link )



L05001

Bacteriophage X glucosyl transferase gene, complete cds

gi|216044|gb|L05001|PXFCLUSYLT [216044]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

M29479

Bacteriophage p4 sid and psu genes partial cds, and delta gene, complete cds gi|215701|

gb|M29479|PP4SDP [215701]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 protein links, or 4 nucleotide neighbors )

SEG\_PP4PSUSID

Bacteriophage P4 capsid size determination protein (sid) gene, 5' end

gi|215698|gb|SEG\_PP4PSUSID [215698]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

M29650

Bacteriophage P4 polarity suppression protein (psu) gene, complete cds

gi|215697|gb|M29650|PP4PSUSID2 [215697]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M29651

Bacteriophage P4 capsid size determination protein (sid) gene, 5' end

gi|215696|gb|M29651|PP4PSUSID1 [215696]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

M27748

Bacteriophage P4 gop, beta, and cII genes, complete cds and int gene, 3' end

gi|215691|gb|M27748|PP4GOPBC [215691]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 1 nucleotide neighbor )

K02750

Bacteriophage IKe, complete genome

gi|215061|gb|K02750|IKECG [215061]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 10 protein links, 4 nucleotide neighbors, or 1 genome link )

L40418

Bacteriophage phi-80 gene, complete cds

gi|1019107|gb|L40418|P80A [1019107]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

AF032122

Bacteriophage SfiI integrase (int) gene, partial cds; and bactoprenol glucosyl transferase (bgt), and glucosyl tranferase II (grtII) genes,complete cds

gi|2465412|gb|AF021347|AF021347 [2465412]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINElink, 4 protein links, or 2 nucleotide neighbors )

M35825

Bacteriophage SF6 fragment D lysozyme gene, complete cds

gi|216105|gb|M35825|SF6LYZ [216105]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 protein link )

Z35479

Bacteriophage C16 ip1 gene

gi|534936|emb|Z35479|BC16IP1 [534936]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 2 nucleotide neighbors )

## X12638

Bacteriophage 21 DNA for gene 2

gi|296141|emb|X12638|B21GENE2 [296141]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## X02501

Bacteriophage 21 DNA for left end sequence with genes 1 and 2

gi|15825|emb|X02501|XXPHA21 [15825]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors )

## M65239

Bacteriophage 21 lysis genes S, R, and Rz, complete cds

gi|215466|gb|M65239|PH2LYSGEN [215466]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

## M58702

Bacteriophage 21 late gene regulatory region

gi|215465|gb|M58702|PH2LATEGE [215465]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## M81255

Bacteriophage 21 head gene operon

gi|215454|gb|M81255|PH2HEADTL [215454]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 10 protein links, or 4 nucleotide neighbors )

## M23775

Bacteriophage 21 glycoprotein 1 gene, complete cds, and glycoprotein gene, 5' end

gi|215451|gb|M23775|PH2GPA [215451]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors )

## M61865

Bacteriophage 21 excisionase (xis), integrase (int) and isocitrate dehydrogenase (icd), complete cds

gi|215448|gb|M61865|PH22XISAA [215448]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 9 nucleotide neighbors )

## S72011

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618967|gb|AF017629|AF017629 [2618967]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017628

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618964|gb|AF017628|AF017628 [2618964]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017627

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds

gi|2618961|gb|AF017627|AF017627 [2618961]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017626

Bacteriophage 21 isocitrate dehydrogenase (icd) gene, partial cds; and integrase (int) gene, partial cds

gi|2618958|gb|AF017626|AF017626 [2618958]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 49 nucleotide neighbors )

## AF017625

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds  
gi|2618955|gb|AF017625|AF017625 [2618955]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017624

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds  
gi|2618952|gb|AF017624|AF017624 [2618952]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017623

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds  
gi|2618949|gb|AF017623|AF017623 [2618949]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017622

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds  
gi|2618946|gb|AF017622|AF017622 [2618946]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## AF017621

Bacteriophage 21 isocitrate dehydrogenase (icd) and integrase (int) genes, partial cds  
gi|2618943|gb|AF017621|AF017621 [2618943]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 44 nucleotide neighbors )

## M57455

Bacteriophage 42D (clone pDB17) (from *Staphylococcus aureus*) staphylokinase gene, complete cds  
gi|215344|gb|M57455|P42STK [215344]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 9 nucleotide neighbors )

## Y12633

Bacteriophage 85 DNA, promoter sequence of unknown gene  
gi|2058285|emb|Y12633|B85PROM [2058285]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## X98146

Bacteriophage P1 DNA sequence around the Op88 operator  
gi|1359513|emb|X98146|BP1OP88OP [1359513]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 nucleotide neighbor )

## Y07739

*Staphylococcus* phage Twort holTW, plyTW genes  
gi|2764979|emb|Y07739|BPTWGHOLG [2764979]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links )

## L07580

Bacteriophage phi-11 rinA and rin B genes, required for the activation of *Staphylococcal* phage phi-11 int expression  
gi|166160|gb|L07580|BPHRINAB [166160]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 2 protein links)

## M34832

Bacteriophage phi-11 integrase (int) and excisionase (xis) genes, complete cds  
gi|166157|gb|M34832|BPHINTXIS [166157]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

M20394

Bacteriophage phi-11 S.aureus attachment site (attP)

gi|166156|gb|M20394|BPHATTP [166156]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 nucleotide neighbors )

X23128

Bacteriophage phi-13 integrase gene

gi|758228|emb|X82312|PHI13INT [758228]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 3 nucleotide neighbors )

X61719

S.aureus phi-13 lysogen right chromosome/bacteriophage DNA junction

gi|46625|emb|X61719|SAP13RJNC [46625]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

X61718

S.aureus phi-13 lysogen left chromosomal/bacteriophage DNA junction

gi|46624|emb|X61718|SAP13LJNC [46624]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

X61717

Bacteriophage phi-13 core sequence for attachment

gi|14799|emb|X61717|BP13ATTP [14799]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, or 3 nucleotide neighbors )

U01875

Bacteriophage phi-13 putative regulatory region and integrase (int) gene, partial cds

gi|437118|gb|U01875|U01875 [437118]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, or 4 nucleotide neighbors )

X67739

S.aureus Bacteriophage phi-42 attP gene

gi|14809|emb|X67739|BPATTPA [14809]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 3 nucleotide neighbors )

U01872

Bacteriophage phi-42 integrase (int) gene, complete cds

gi|437115|gb|U01872|U01872 [437115]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 2 protein links, or 3 nucleotide neighbors )

X94423

Staphylococcus aureus bacteriophage phi-42 DNA with ORFs (restriction modification system)

gi|1771597|emb|X94423|SARMS [1771597]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 1 nucleotide neighbor )

M27965

Bacteriophage L54a (from S.aureus) int and xis genes, complete cds

gi|215096|gb|M27965|L54INTXIS [215096]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, MEDLINE 1 link, 2 protein links, or 3 nucleotide neighbors )

U72397

Bacteriophage 80 alpha holin and amidase genes, complete cds

gi|1763241|gb|U72397|B8U72397 [1763241]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 2 nucleotide neighbors )

## AB009866

Bacteriophage phi PVL proviral DNA, complete sequence

gi|3341907|dbj|AB009866|AB009866 [3341907]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,63 protein links, or 1 nucleotide neighbor )

## Z47794

Bacteriophage Cp-1 DNA, complete genome

gi|2288892|emb|Z47794|BPCP1XX [2288892]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 28 protein links, 1 nucleotide neighbor, or 1 genome link )

## SEG\_CP7RSIT

Bacteriophage Cp-7 (S.pneumoniae) 5' inverted terminal repeat

gi|166186|gb|SEG\_CP7RSIT [166186]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## M11635

Bacteriophage Cp-7 (S.pneumoniae) DNA, 3' inverted terminal repeat

gi|166185|gb|M11635|CP7RSIT2 [166185]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## M11636

Bacteriophage Cp-7 (S.pneumoniae) 5' inverted terminal repeat

gi|166184|gb|M11636|CP7RSIT1 [166184]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## SEG\_CP5RSIT

Bacteriophage Cp-5 (S.pneumoniae), 5' inverted terminal repeat

gi|166181|gb|SEG\_CP5RSIT [166181]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1 MEDLINE link )

## M11633

Bacteriophage Cp-5 (S.pneumoniae) 3' inverted terminal repeat

gi|166180|gb|M11633|CP5RSIT2 [166180]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## M11634

Bacteriophage Cp-5 (S.pneumoniae), 5' inverted terminal repeat

gi|166179|gb|M11634|CP5RSIT1 [166179]

(View GenBank report,FASTA report,ASN.1 report, or Graphical view)

## M34780

Bacteriophage Cp-9 muramidase (cp19) gene

gi|166187|gb|M34780|CP9CPL [166187]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 1 nucleotide neighbor )

## M34652

Bacteriophage HB-3 amidase (hbl) gene, complete cds

gi|215055|gb|M34652|HB3HBLA [215055]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

## U64984

Streptococcus pyogenes phage T12 repressor, excisionase (xis), integrase(int) and erythrogenic toxin A precursor (speA) genes, complete cds gi|1877426|gb|U40453|SPU40453 [1877426]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 4 protein links, or 22 nucleotide neighbors )

## X12375

Phage CP-T1 (*Vibrio cholerae*) DNA for packaging signal (pac site)

gi|15435|emb|X12375|NCCPPAC [15435]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

## AF087814

*Vibrio cholerae* filamentous bacteriophage fs-2 DNA, complete genome sequence

gi|3702207|dbj|AB002632|AB002632 [3702207]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 9 protein links, or 1 genome link )

## D83518

Bacteriophage KVP40 gene for major capsid protein precursor, complete cds

gi|3046858|dbj|D83518|D83518 [3046858]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

## AF033322

Bacteriophage PST single-stranded binding protein (gene 32) gene, partial cds, and 5' region

gi|2645774|gb|AF033322|AF033322 [2645774]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 protein link, or 17 nucleotide neighbors )

## X94331

Bacteriophage L cro, 24, c2, and c1 genes

gi|1469213|emb|X94331|BLCRO24C [1469213]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 4 protein links )

## U82619

*Shigella flexneri* bacteriophage V glucosyl transferase (gtr), integrase (int) and excisionase (xis) genes, complete cds

gi|2465470|gb|U82619|SFU82619 [2465470]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 8 protein links, or 1 nucleotide neighbor )

**NCBI *Entrez* Nucleotide QUERY**

**Key words: bacteriophage and lysis**

**56 citations found (all selected)**

AJ011581

Bacteriophage PS119 lysis genes 13, 19, 15, and packaging gene 3, complete cds  
gil3676084|embl|AJ011581|BPS011581 [3676084]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 protein links, or 1 nucleotide neighbor )

AJ011580

Bacteriophage PS34 lysis genes 13, 19, 15, antiterminator gene 23, and packaging gene 3, complete cds  
gil3676078|embl|AJ011580|BPS011580 [3676078]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,5 protein links, or 2 nucleotide neighbors )

AJ011579

Bacteriophage PS3 lysis genes 13, 19, 15, and packaging gene 3  
gil3676073|embl|AJ011579|BPS011579 [3676073]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 protein links, or 1 nucleotide neighbor )

AF034975

Bacteriophage H-19B essential recombination function protein (erf), kil protein (kil), regulatory protein cIII (cIII), protein gp17 (17), N protein (N), cI protein (cI), cro protein (cro), cII protein (cII), O protein (O), P protein (P), ren protein (ren), Roi (roi), Q protein (Q), Shiga-like toxin A (slt-IA) and B (slt-IB) subunits, and putative holin protein (S) genes, complete cds  
gil2668751|gb|AF034975| [2668751]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 20 protein links, or 30 nucleotide neighbors )

U37314

Bacateriophage lambda Rz1 protein precursor (Rz1) gene, complete cds  
gil1017780|gb|U37314|BLU37314 [1017780]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 1 protein link, or 9 nucleotide neighbors )

U00005

E. coli hflA locus encoding the hflX, hflK and hflC genes, hfq gene, complete cds; miaA gene, partial cds  
gil436153|gb|U00005|ECOHLA [436153]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 MEDLINE

links, 5 protein links, or 8 nucleotide neighbors )

#### U32222

Bacteriophage 186, complete sequence

gi|3337249|gb|U32222|B1U32222 [3337249]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 46 protein links, or 5 nucleotide neighbors )

#### AF064539

Bacteriophage N15, complete genome

gi|3192683|gb|AF064539|AF064539 [3192683]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 60 protein links, 26 nucleotide neighbors, or 1 genome link )

#### AF063097

Bacteriophage P2, complete genome

gi|3139086|gb|AF063097|AF063097 [3139086]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,21 MEDLINE links, 42 protein links, 3 nucleotide neighbors, or 1 genome link )

#### Z97974

Bacteriophage phiadh lys, hol, intG, rad,and tec genes

gi|2707950|emb|Z97974|BPHIADH [2707950]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 9 protein links, or 1 nucleotide neighbor )

#### AF059243

Bacteriophage NL95, complete genome

gi|3088545|gb|AF059243|AF059243 [3088545]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 4 protein links, 3 nucleotide neighbors, or 1 genome link )

#### AF052431

Bacteriophage M11 A-protein, coat protein, A1-protein, and replicase genes, complete cds

gi|2981208|gb|AF052431| [2981208]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 4 protein links, or 8 nucleotide neighbors )

#### Y07739

Staphylococcus phage Twort holTW, plyTW genes

gi|2764979|emb|Y07739|BPTWGHOLG [2764979]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links )

#### X94331



Bacteriophage L cro, 24, c2, and c1 genes  
 gil1469213|emblX94331|BLCRO24C [1469213]  
 (View GenBank report, FASTA report, ASN.1 report, Graphical view, 1 MEDLINE link, or 4 protein links )

X78410

Bacteriophage phiadh holin and lysin genes  
 gil793848|emblX78410|LGHOLLYS [793848]  
 (View GenBank report, FASTA report, ASN.1 report, Graphical view, 1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

X99260

Bacteriophage B103 genomic sequence  
 gil1429229|emblX99260|BB103G [1429229]  
 (View GenBank report, FASTA report, ASN.1 report, Graphical view, 1 MEDLINE link, 17 protein links, or 12 nucleotide neighbors )

AJ000741

Bacteriophage P1 darA operon  
 gil2462938|emblAJ000741|BPAJ7641 [2462938]  
 (View GenBank report, FASTA report, ASN.1 report, Graphical view, 1 MEDLINE link, 10 protein links, or 31 nucleotide neighbors )

X87420

Bacteriophage ES18 genes 24, c2, cro, c1, 18, and oL and oR operators  
 gil1143407|emblX87420|BPES18GEN [1143407]  
 (View GenBank report, FASTA report, ASN.1 report, Graphical view, 5 protein links, or 9 nucleotide neighbors )

L35561

Bacteriophage phi-105 ORFs 1-3  
 gil532218|gbL35561|PH5ORFHTR [532218]  
 (View GenBank report, FASTA report, ASN.1 report, Graphical view, 1 MEDLINE link, or 3 protein links )

D10027

Group II RNA coliphage GA genome  
 gil217784|dbjD10027|PGAXX [217784]  
 (View GenBank report, FASTA report, ASN.1 report, Graphical view, 1 MEDLINE link, 3 protein links, 5 nucleotide neighbors, or 1 genome link )

V01128

Bacteriophage phi-X174 (cs70 mutation) complete genome  
 gil15535|emblV01128|PHIX174 [15535]  
 (View GenBank report, FASTA report, ASN.1 report, Graphical view, 4 MEDLINE links, 11 protein links, or 26 nucleotide neighbors )

S81763

coat gene...replicase gene [bacteriophage KU1, host=Escherichia coli,  
group II RNA phage, Genomic RNA, 3 genes, 120 nt]  
gil1438766|gb|S81763|S81763 [1438766]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 1  
MEDLINE link )

U38906

Bacteriophage r1t integrase, repressor protein (rro), dUTPase, holin and  
lysin genes, complete cds  
gil1353517|gb|U38906|BRU38906 [1353517]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE  
links, 50 protein links, or 3 nucleotide neighbors )

X91149

Bacteriophage phi-C31 DNA cos region  
gil1107473|emb|X91149|APHIC31C [1107473]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE  
link, 6 protein links, or 1 nucleotide neighbor )

V00642

phage MS2 genome  
gil15081|emb|V00642|LEMS2X [15081]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,8 MEDLINE  
links, 4 protein links, or 20 nucleotide neighbors )

V01146

Genome of bacteriophage T7  
gil431187|emb|V01146|T7CG [431187]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,13 MEDLINE  
links, 60 protein links, 105 nucleotide neighbors, or 1 genome link )

X78401

Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin  
region genes, ninG phosphatase, late control gene 23, orf 60, complete  
cds, late control region, start of lysis gene 13  
gil512343|emb|X78401|POP22NIN [512343]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE  
links, 13 protein links, or 4 nucleotide neighbors )

Y00408

Bacteriophage T4 gene t for lysis protein  
gil15368|emb|Y00408|MYT4T [15368]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE  
link, 1 protein link, or 3 nucleotide neighbors )

Z26590

662021 " 2543463

Bacteriophage mv4 lysA and lysB genes  
 gil410500|emb|Z26590|MV4LYSAB [410500]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view, or 4 protein links )

X07809

Phage phiX174 lysis (E) gene upstream region  
 gil15094|emb|X07809|MIPHIXE [15094]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 4 nucleotide neighbors )

Z34528

Lactococcal bacteriophage c2 lysin gene  
 gil506455|emb|Z34528|LBC2LYSIN [506455]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 4 nucleotide neighbors )

X15031

Bacteriophage fr RNA genome  
 gil15071|emb|X15031|LEBFRX [15071]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, 9 nucleotide neighbors, or 1 genome link )

X80191

Bacteriophage PP7 mRNA for maturation, coat, lysis and replicase proteins  
 gil517237|emb|X80191|BPP7PR [517237]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 1 genome link )

X85010

Bacteriophage A511 ply511 gene  
 gil853748|emb|X85010|BPA511PLY [853748]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

X85009

Bacteriophage A500 hol500 and ply500 genes  
 gil853744|emb|X85009|BPA500PLY [853744]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 4 nucleotide neighbors )

X85008

Bacteriophage A118 hol118 and ply118 genes  
 gil853740|emb|X85008|BPA118PLY [853740]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

Z35638

Bacteriophage phi-X174 genes for lysis protein and beta-lactamase  
 gi|520996|emb|Z35638|BPLYSPR [520996]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE  
 link, 2 protein links, or 516 nucleotide neighbors )

J02459

Bacteriophage lambda, complete genome  
 gi|215104|gb|J02459|LAMCG [215104]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,87 MEDLINE  
 links, 67 protein links, 190 nucleotide neighbors, or 1 genome link )

X87674

Bacteriophage P1 lydA & lydB genes  
 gi|974763|emb|X87674|BACP1LYD [974763]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE  
 link, 2 protein links, or 2 nucleotide neighbors )

X87673

Bacteriophage P1 gene 17  
 gi|974761|emb|X87673|BACP117 [974761]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE  
 link, 1 protein link, or 1 nucleotide neighbor )

M14784

Bacteriophage T3 strain amNG220B right end, tail fiber protein, lysis  
 protein and DNA packaging proteins, complete cds  
 gi|215810|gb|M14784|PT3RE [215810]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE  
 link, 9 protein links, or 10 nucleotide neighbors )

M11813

Bacteriophage PZA (from B.subtilis), complete genome  
 gi|216046|gb|M11813|PZACG [216046]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE  
 links, 27 protein links, 17 nucleotide neighbors, or 1 genome link )

M16812

Bacteriophage K3 't' lysis gene, complete cds  
 gi|215503|gb|M16812|PK3LYST [215503]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE  
 link, 1 protein link, or 4 nucleotide neighbors )

J04356

Bacteriophage P22 proteins 15 (complete cds), and 19 (3' end) genes  
 gi|215265|gb|J04356|P2215P [215265]

66224463

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 2 nucleotide neighbors )

## J04343

Bacteriophage JP34 coat and lysis protein genes, complete cds, and replicase protein gene, 5' end  
gil215076|gb|J04343|JP3COLY [215076]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 2 nucleotide neighbors )

## J02482

Bacteriophage phi-X174, complete genome  
gil216019|gb|J02482|PX1CG [216019]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,23 MEDLINE links, 11 protein links, 26 nucleotide neighbors, or 1 genome link )

## M99441

Bacteriophage T4 anti-sigma 70 protein (asiA) gene, complete cds and lysis protein, 3' end  
gil215820|gb|M99441|PT4ASIA [215820]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 2 protein links, or 2 nucleotide neighbors )

## M65239

Bacteriophage 21 lysis genes S, R, and Rz, complete cds  
gil215466|gb|M65239|PH2LYSGEN [215466]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

## M10637

Phage G4 D/E overlapping gene system, encoding D (morphogenetic) and E (lysis) proteins

gil215427|gb|M10637|PG4DE [215427]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 12 nucleotide neighbors )

## J02454

Bacteriophage G4, complete genome

gil215415|gb|J02454|PG4CG [215415]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 11 protein links, 20 nucleotide neighbors, or 1 genome link )

## J02580

Bacteriophage PA-2 (E.coli porcine strain isolate) Rz gene, 5'end; ORF2, outer membrane porin protein (Ic) and ORF1 genes, complete cds  
gil215366|gb|J02580|PA2LC [215366]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 4 nucleotide neighbors )

## M14782

Bacillus phage phi-29 head morphogenesis, major head protein, head fiber protein, tail protein, upper collar protein, lower collar protein, pre-neck appendage protein, morphogenesis(13), lysis, morphogenesis(15), encapsidation genes, complete cds  
 gi|215323|gb|M14782|P29LATE2 [215323]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 11 protein links, or 11 nucleotide neighbors )

## M10997

Bacteriophage P22 lysis genes 13 and 19, complete cds  
 gi|215262|gb|M10997|P221319 [215262]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 3 nucleotide neighbors )

## J02467

Bacteriophage MS2, complete genome  
 gi|215232|gb|J02467|MS2CG [215232]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,8 MEDLINE links, 4 protein links, 20 nucleotide neighbors, or 1 genome link )

## M14035

Bacteriophage lambda lysis S gene with mutations leading to nonlethality of S in the plasmid pRG1  
 gi|215180|gb|M14035|LAMLYS [215180]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 14 nucleotide neighbors )

## U04309

Bacteriophage phi-LC3 putative holin (lysA) gene and putative murein hydrolase (lysB) gene, complete cds  
 gi|530796|gb|U04309|BPU04309 [530796]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

## NCBI *Entrez* Nucleotide QUERY

**Key word: holin**

**51 citations found (all selected)**

AF034975

Bacteriophage H-19B essential recombination function protein (erf), kil protein (kil), regulatory protein cIII (cIII), protein gp17 (17), N protein (N), cI protein (cI), cro protein (cro), cII protein (cII), O protein (O), P protein (P), ren protein (ren), Roi (roi), Q protein (Q), Shiga-like toxin A (slt-IA) and B (slt-IB) subunits, and putative holin protein (S) genes, complete cds  
gil2668751|gb|AF034975| [2668751]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 20 protein links, or 30 nucleotide neighbors )

U52961

Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds  
gil1841516|gb|U52961|SAU52961 [1841516]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

U28154

Haemophilus somnus cryptic prophage genes, capsid scaffolding protein gene, partial cds, major capsid protein precursor, endonuclease, capsid completion protein, tail synthesis proteins, holin, and lysozyme genes, complete cds  
gil1765928|gb|U28154|HSU28154 [1765928]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 13 protein links )

AF032122

Streptococcus thermophilus bacteriophage Sfi19 central region of genome  
gil2935682|gb|AF032122| [2935682]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 14 protein links, or 2 nucleotide neighbors )

AF032121

Streptococcus thermophilus bacteriophage Sfi21 central region of genome  
gil2935667|gb|AF032121|AF032121 [2935667]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 14 protein links, or 2 nucleotide neighbors )

66232122121

Bacillus subtilis 168 prophage SPbeta N-acetylmuramoyl-L-alanine amidase (blyA), holin-like protein (bhlA), holin-like protein (bhlB), and yolK genes, complete cds; and yolJ gene, partial cds  
gi|2997594|gb|AF021803|AF021803 [2997594]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 5 protein links, or 1 nucleotide neighbor)

Streptococcus thermophilus bacteriophage sfi11 gp502 (orf502), gp284 (orf284), gp129 (orf129), gp193 (orf193), gp119 (orf119), gp348 (orf348), gp53 (orf53), gp113 (orf113), gp104 (orf104), gp114 (orf114), gp128 (orf128), gp168 (orf168), gp117 (orf117), gp105 (orf105), putative minor tail protein (orf1510), putative minor structural protein (orf512), putative minor structural protein (orf1000), gp373 (orf373), gp57 (orf57), putative anti-receptor (orf695), putative minor structural protein (orf669), gp149 (orf149), putative holin (orf141), putative holin (orf87), and lysin (orf288) genes, complete cds  
gi|3320432|gb|AF057033|AF057033 [3320432]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,25 protein links, or 1 nucleotide neighbor )

**Bacteriophage 186, complete sequence**  
gi|3337249|gb|U32222|B1U32222 [3337249]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE  
links, 46 protein links, or 5 nucleotide neighbors )

**Bacteriophage phi PVL proviral DNA, complete sequence**  
gi|3341907|dbj|AB009866|AB009866 [3341907]  
(View GenBank report, FASTA report, ASN.1 report, Graphical view, 63 protein links, or 1 nucleotide neighbor)

**Bacteriophage bIL170, complete genome**  
 gil3282260|gb|AF009630|AF009630 [3282260]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,63 protein  
 links, 3 nucleotide neighbors, or 1 genome link )

## Bacteriophage N15, complete genome



gi|3192683|gb|AF064539|AF064539 [3192683]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE  
 links, 60 protein links, 26 nucleotide neighbors, or 1 genome link )

AF063097

Bacteriophage P2, complete genome  
 gi|3139086|gb|AF063097|AF063097 [3139086]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,21 MEDLINE  
 links, 42 protein links, 3 nucleotide neighbors, or 1 genome link )

Z97974

Bacteriophage phiadh lys, hol, intG, rad, and tec genes  
 gi|2707950|emb|Z97974|BPHIADH [2707950]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE  
 links, 9 protein links, or 1 nucleotide neighbor )

X95646

Streptococcus thermophilus bacteriophage Sfi21 DNA; lysogeny module,  
 8141 bp  
 gi|2292747|emb|X95646|BSFI21LYS [2292747]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE  
 links, 19 protein links, or 3 nucleotide neighbors )

SEG\_LLHLYSINO

Bacteriophage LL-H structural protein gene, partial cds; minor  
 structural protein gp61 (g57), unknown protein, unknown protein,  
 structural protein (g20), unknown protein, unknown protein, major capsid  
 protein (g34), main tail protein gp19 (g17), holin (hol), muramidase  
 (mur), unknown protein, unknown protein, unknown protein, unknown  
 protein, unknown protein, and unknown protein genes, complete cds;  
 unknown protein gene, partial cds; and unknown protein, unknown protein,  
 unknown protein, unknown protein, unknown protein, minor structural  
 protein gp75 (g70), minor structural protein gp89 (g88), minor  
 structural protein gp58 (g71), unknown protein, unknown protein, unknown  
 protein, and unknown protein genes, complete cds  
 gi|1004337|gb|SEG\_LLHLYSINO [1004337]  
 (View GenBank report,FASTA report,ASN.1 report,Graphical view,4 MEDLINE  
 links, 31 protein links, or 1 nucleotide neighbor )

M96254

Bacteriophage LL-H holin (hol), muramidase (mur), and unknown protein  
 genes, complete cds  
 gi|1004336|gb|M96254|LLHLYSINO3 [1004336]  
 (View GenBank report,FASTA report,ASN.1 report, or Graphical view)

552327 " 25245450

Y07740

Staphylococcus phage 187 ply187 and hol187 genes  
 gil2764982|embl|Y07740|BP187PLYH [2764982]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 2 protein links )

U88974

Streptococcus thermophilus bacteriophage 01205 DNA sequence  
 gil2444080|gb|U88974| [2444080]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 57 protein links, or 6 nucleotide neighbors )

Z99117

Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870

gil2634966|embl|Z99117|BSUB0014 [2634966]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,233 protein links, 51 nucleotide neighbors, or 1 genome link )

Z99115

Bacillus subtilis complete genome (section 12 of 21): from 2195541 to 2409220

gil2634478|embl|Z99115|BSUB0012 [2634478]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,244 protein links, 64 nucleotide neighbors, or 1 genome link )

Z99110

Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140

gil2633472|embl|Z99110|BSUB0007 [2633472]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,226 protein links, 31 nucleotide neighbors, or 1 genome link )

X78410

Bacteriophage phiadh holin and lysin genes

gil793848|embl|X78410|LGHOLLYS [793848]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

Z93946

Lactobacillus bacteriophage phig1e complete genomic DNA  
gi|1926320|emb|X98106|LBPHIG1E [1926320]  
(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE

link, 50 protein links, or 4 nucleotide neighbors )

U72397

Bacteriophage 80 alpha holin and amidase genes, complete cds

gi|1763241|gb|U72397|B8U72397 [1763241]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 protein links, or 2 nucleotide neighbors )

U38906

Bacteriophage r1t integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds

gi|1353517|gb|U38906|BRU38906 [1353517]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 50 protein links, or 3 nucleotide neighbors )

X91149

Bacteriophage phi-C31 DNA cos region

gi|1107473|emb|X91149|APHIC31C [1107473]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 6 protein links, or 1 nucleotide neighbor )

U24159

Bacteriophage HP1 strain HP1c1, complete genome

gi|1046235|gb|U24159|BHU24159 [1046235]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,6 MEDLINE links, 41 protein links, 8 nucleotide neighbors, or 1 genome link )

Z26590

Bacteriophage mv4 lysA and lysB genes

gi|410500|emb|Z26590|MV4LYSAB [410500]

(View GenBank report,FASTA report,ASN.1 report,Graphical view, or 4 protein links )

Z70177

B.subtilis DNA (28 kb PBSX/skin element region)

gi|1225934|emb|Z70177|BSPBSXSE [1225934]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,32 protein links, or 4 nucleotide neighbors )

Z36941

65 27 0 2 7 " 23 53 22 5 4 6 3

B.subtilis defective prophage PBSX xhlA, xhlB, and xylA genes

gi|535793|emb|Z36941|BSPBSXXHL [535793]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,4 protein links, or 5 nucleotide neighbors )

X89234

L.innocua DNA for phagelysin and holin gene

gi|1134844|emb|X89234|LICPLYHOL [1134844]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 4 nucleotide neighbors )

X85010

Bacteriophage A511 ply511 gene

gi|853748|emb|X85010|BPA511PLY [853748]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

X85009

Bacteriophage A500 hol500 and ply500 genes

gi|853744|emb|X85009|BPA500PLY [853744]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 4 nucleotide neighbors )

X85008

Bacteriophage A118 hol118 and ply118 genes

gi|853740|emb|X85008|BPA118PLY [853740]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

L34781

Bacteriophage phi 11 holin homologue (ORF3) gene, complete cds and

peptidoglycan hydrolase (lytA) gene, partial cds

gi|511838|gb|L34781|BPHHOLIN [511838]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 4 protein links, or 2 nucleotide neighbors )

U11698

Serratia marcescens SM6 extracellular secretory protein (nucE), putative

phage lysozyme (nucD), and transcriptional activator (nucC) genes,

complete cds

gi|509550|gb|U11698|SMU11698 [509550]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE

094545 12099

link, 3 protein links, or 1 nucleotide neighbor )

### U31763

*Serratia marcescens* phage-holin analog protein (regA), putative phage lysozyme (regB), and transcriptional activator (regC) genes, complete cds

gi|965068|gb|U31763|SMU31763 [965068]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 3 protein links, or 1 nucleotide neighbor )

### X87674

Bacteriophage P1 lydA & lydB genes

gi|974763|emb|X87674|BACP1LYD [974763]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 2 nucleotide neighbors )

### L48605

Bacteriophage c2 complete genome

gi|1146276|gb|L48605|C2PVCG [1146276]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,3 MEDLINE links, 39 protein links, 3 nucleotide neighbors, or 1 genome link )

### L33769

Bacteriophage bIL67 DNA polymerase subunit (ORF3-5), essential recombination protein (ORF13), lysin (ORF24), minor tail protein (ORF31), terminase subunit (ORF32), holin (ORF37), unknown protein (ORF 1-2,6-12,14-23,25-30,33-36), complete genome

gi|522252|gb|L33769|L67CG [522252]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 37 protein links, 2 nucleotide neighbors, or 1 genome link )

### L31348

Bacteriophage Tuc2009 integrase (int) gene, complete cds; lysin (lys) gene, 3' end

gi|508612|gb|L31348|TU2INT [508612]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 3 protein links, or 3 nucleotide neighbors )

### L31364

Bacteriophage Tuc2009 holin (S) gene, complete cds; lysin (lys) gene, complete cds

gi|496281|gb|L31364|TU2SLYS [496281]

662021 25243450

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

**L31366**

Bacteriophage Tuc2009 structural protein (mp2) gene, complete cds

gi|496278|gb|L31366|TU2MP2A [496278]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

**L31365**

Bacteriophage Tuc2009 structural protein (mp1) gene, complete cds

gi|496276|gb|L31365|TU2MP1A [496276]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, or 1 protein link )

**U04309**

Bacteriophage phi-LC3 putative holin (lysA) gene and putative murein hydrolase (lysB) gene, complete cds

gi|530796|gb|U04309|BPU04309 [530796]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 2 protein links, or 1 nucleotide neighbor )

530796 " 2245450

**NCBI Entrez Nucleotide QUERY****Key word: bacteriophage and kil****5 citations found (all selected)**

AF034975

Bacteriophage H-19B essential recombination function protein (erf), kil protein (kil), regulatory protein cIII (cIII), protein gp17 (17), N protein (N), cI protein (cI), cro protein (cro), cII protein (cII), O protein (O), P protein (P), ren protein (ren), Roi (roi), Q protein (Q), Shiga-like toxin A (slt-IA) and B (slt-IB) subunits, and putative holin protein (S) genes, complete cds

gi|2668751|gb|AF034975| [2668751]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 20 protein links, or 30 nucleotide neighbors )

X15637

Bacteriophage P22 P(L) operon encompassing ral, 17, kil and arf genes

gi|156461|emb|X15637|POP22PL [15646]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 7 protein links, or 2 nucleotide neighbors )

J02459

Bacteriophage lambda, complete genome

gi|215104|gb|J02459|LAMCG [215104]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,87 MEDLINE links, 67 protein links, 190 nucleotide neighbors, or 1 genome link )

M64097

Bacteriophage Mu left end

gi|215543|gb|M64097|PMULEFTEN [215543]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,2 MEDLINE links, 39 protein links, or 15 nucleotide neighbors )

M18902

Bacteriophage D108 kil gene encoding a replication protein, 3' end; and containing three ORFs, complete cds

gi|166191|gb|M18902|D18KIL [166191]

(View GenBank report,FASTA report,ASN.1 report,Graphical view,1 MEDLINE link, 1 protein link, or 3 nucleotide neighbors )

662022 " 25243450